Fig. 1

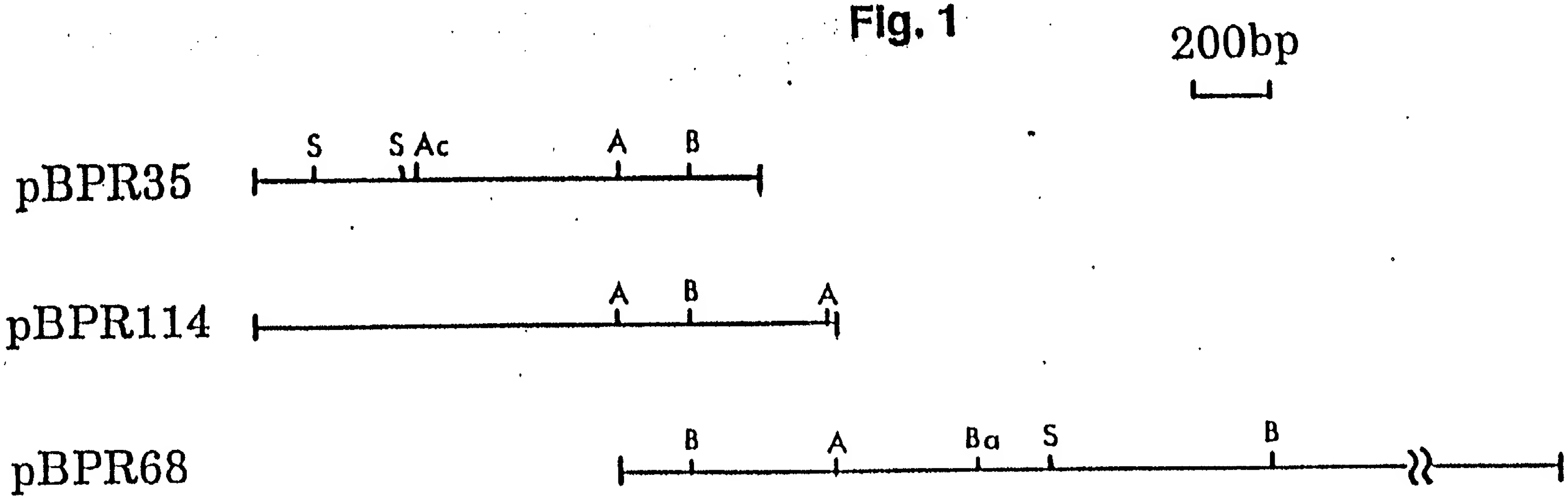

Fig. 2

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1     TGGCCTGCACCCCACCCCCCAGCCTGCGAAGACGGGGGAGGCGGTGGTCGGTCGCCTCCCTCCTGCCCCCGGCCTGGCTTCGCGGTGGAG   91
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184   GCGGCGACTGACAGCGGCGGCGGCGGCGGCAGCGGCTCCAAGGCGAGCGTGGTCCCCGCGTGCGCACAAGCTCGCCGCCGCGCAGGGACCCA   275
276   CGGACACCGGCGCCCGGGCGGACACACAGACGCGGAGATCGGGCTCTACGCGCGCTACTCAGCGCACGAGCTCCCCATCCCTGGGCGGAGCGG   367
368   GGCGCGGACTCGCCGCTGCGCGCCCTCCCCGCGGAGTCTGCCCCGGGCAGACCCGCAGCCCCGCGGCCCCGCCGCGAGGCCCCTCGGTGAGCA   459

1                                                 Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg   13
460   GCCTGTAGACACCTGGGGTTGAGCAGTGGCGGCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT TGC AGG   536

14    Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr   36
537   CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC ACC   605

37    Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn   59
606   GCC ATG CAT TCC GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT   674

60    Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys   82
675   GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG   743

83    Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln   105
744   CCC GCC CAC GTG GGT GAG ATG GTC CTG GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA   812

106   Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met   128
813   GTC TGG GAG ACC GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG   881

129   Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys   151
882   AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT   950

152   Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr   174
951   GGG TTT GAG GAG TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG GCC CTG TAC   1019

175   Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys   197
1020  ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG   1088

198   Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val   220
1089  CTG CAC TGC ACC CGC AAC TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC   1157

221   Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys   243
1158  TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC   1226

244   Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu   266
1227  AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG   1295

267   Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile   289
1296  TAT CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATC ATT   1364

290   Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly   312
1365  GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC   1433

313   Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met   335
1434  TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG   1502

336   Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly   358
1503  GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA   1571

359   Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala Gln Gln   381
1572  GGC AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG CCA CAG CGG GCT CAG CAG   1640

382   His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile   404
1641  CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC   1709

405   Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu   427
1710  CCA CTC TTT GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG   1778

428   Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly   450
1779  GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA   1847

451   Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe   473
1848  GAG GTG CAG GCG GAG ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC   1916

474   Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys   496
1917  AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG   1985

497   Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***   513
1986  AGC AGC TCC CAG ATC CGC ATG TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGA GCCCACCCTGCCCCCTCCTC   2059

2060  TCCTCTGTACGCAGGCTGGGGCTGTGGTGGGGCGCCGGCCCACGCATGTTGTGCCTCTTCTCGCCTTCGGGCAGGCCCCGGGCTGGCCCCT   2151
2152  GGCCCCCGAGGTTGGAGAAGGATGCGGGACAGGCAGCTGTTTAGCCTTCCTGTTTTGGCGCTGGCCCAACCACCGTGGGTCCCTGGGCCTGC   2243
2244  ACCCAGACATGTAATACTCCTTAATTGGGAAGTCATCCATTCTTTCCCTTTCCCAAGTCCTTGCTTATTAAGAGGTTCAAGTCACCTACCCA   2335
2336  ATTCAGAAGCTTAAGTAACCACTAACCACGGTGACTGCGTGGGAGGCCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCCTTGGGCT   2427
2428  GGGGCCCTCCTTAAAGCCCCCCCTGAAATTGTCGGACCTCAAAGTGTGACTCCTTTGAGTCTACTCGCCACCCCCGTGGCCCTTTGCAGCCC   2519
2520  TGGTCCAGTCACCGAGGTTACTGGAAGTCCAGCTTGGATGGCCAGACAGCTTTTTGGCACAGGCAGACCCATGCTCACCCAACATTTTAGTG   2611
2612  TCCAGGTGCCCAGGTGCCCAGGTGCCCAGCTCCTGGGCATCAGACAGTGGGAAAGCTCCAGGGATCTACCATTCAGAGACTTCAGTTTGGAT   2703
2704  GTAGGGCTAAGGCCAGAGAAAAGTTCTGGAGCTTTTCATTTGGCCCAAGAAAAAACTGCCAAGATCCAGAAAAGTGGATCTGAGTGGAATTT   2795
2796  AGATGCAAAGAGCTTGGAG   2814
```

Fig. 3

```
1     TGGCCTGCACCCCACCCCCCAGCCTGCGAAGACGGGGGCAGGCGGTGGTCGGTCGCCTCCCTCCTGCCCCCGGCCTGGCTTCGCGGTCGAG   91
92    GCGGTGCCTCTCCGGCAAGGCAGACCAGGCTGGGCGGACGCGCCGGCGCGGGCGGGCTAGGGAAGGCCGGGGGCCTCGCGCTCGGCCCCCGG   183
184   GCGGCCGACTGACAGCGGCGGCGGCGGCGGCAGCGGCTCCAAGGCGAGCGTGGTCCCCGCGTGCGCACAAGCTCGCCGCCGCGCAGGGACCCA   275
276   CGGACACCGGCGCCCGGGCGGACACACAGACGCGGAGATCGGGCTCTACGCGCGCTACTCAGCGCACGAGCTCCCCATCCCTGGCCCGAGCGG   367
368   GGCGCGGACTCGCCGCTGCGCGCCCTCCCCGCGGAGTCTGCCCCGGGCAGACCCGCAGCCCCGCGCCCCCGCCGCGAGGCCCCTCGGTGAGCA   459
1                                               Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg       13
460   GCCTGTAGACACCTGGGGTTGAGCAGTGGCGGCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT TGC AGG         536
14    Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr      36
537   CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC ACC      605
37    Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn      59
606   GCC ATG CAT TCC GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT      674
60    Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys      82
675   GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG      743
83    Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln      105
744   CCC GCC CAC GTG GGT GAG ATG GTC CTG GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA      812
106   Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met      128
813   GTC TGG GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG      881
129   Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys      151
882   AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT      950
152   Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr      174
951   GGG TTT GAG GAG TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG GCC CTG TAC      1019
175   Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys      197
1020  ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG      1088
198   Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val      220
1089  CTG CAC TGC ACC CGC AAC TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC      1157
221   Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys      243
1158  TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC      1226
244   Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu      266
1227  AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG      1295
267   Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile      289
1296  TAT CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATC ATT      1364
290   Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly      312
1365  GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC      1433
313   Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met      335
1434  TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG      1502
336   Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly      358
1503  GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA      1571
359   Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile      381
1572  GGC AAC GAG TCC AGC ATC TAC TTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT GGA ATC      1640
382   His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly      404
1641  CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG GTG TTT GAG CTG GGT      1709
405   Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu      427
1710  CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG      1778
428   Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro      450
1779  ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC AAG CAC CGG CAC CCA      1847
451   Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile      473
1848  TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC      1916
474   Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***                                             485
1917  CGC ATG TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGA GCCCACCCTGCCCCCTCCTCTCCTCTGTACGCAGGCTGGG   1995
1996  GCTGTGGTGGGGCGCCGGCCCACGCATGTTGTGCCTCTTCTCGCCTTCGGGCAGGCCCCGGGCTGGGCGCCTCGCCCCCGAGGTTGGAGAAG   2087
2088  GATGCGGGACAGGCAGCTGTTTAGCCTTCCTGTTTTGGCGCTGGCCCAACCACCGTGGGTCCCTGGCCCTGCACCCAGACATGTAATACTCC   2179
2180  TTAATTGGGAAGTCATCCATTCTTTCCCTTTCCCAAGTCCTTGCTTATTAAGAGGTTCAAGTCACCTACCCAATTCAGAAGCTTAAGTAACC   2271
2272  ACTAACCACCGTGACTGCGTGGGAGGCCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCCTTGGGCTGGGGCCCTCCTTAAAGCCCC   2363
2364  CCCTGAAATTGTCGGACCTCAAAGTGTGACTCCTTTGAGTCTACTCGCCACCCCCGTGGCCCTTTGCAGCCCTGGTCCAGTCACCGAGGTTA   2455
2456  CTGGAAGTCCAGCTTGGATGGCCAGACAGCTTTTTGGCACAGGCAGACCCATGCTCACCCAACATTTTAGTGTCCAGGTGCCCAGGTGCCCA   2547
2548  GGTGCCCAGCTCCTGGGCATCAGACAGTGGCAAAGCTCCAGGGATCTACCATTCAGAGACTTCAGTTTGGATGTAGGGCTAAGGCCAGAGAA   2639
2640  AAGTTCTGGAGCTTTTCATTTGGCCCAAGAAAAAACTGCCAAGATCCAGAAAAGTGGATCTGAGTGGAATTTAGATGCAAAGAGCTTGGAG   2730
```

Fig. 4

	1				5					10	
Bovine cDNA	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln
	*	*	*	*	*	*	*	*	*	*	*
Purified bovine Sample	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln

			15					20					25
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met
*	*	*	*	*	*	*	*	*	*	*	*	*	*
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met

Gly	Leu	Asn	Asp
*	*	*	*
Gly	Leu	Asn	Asp

Fig. 5

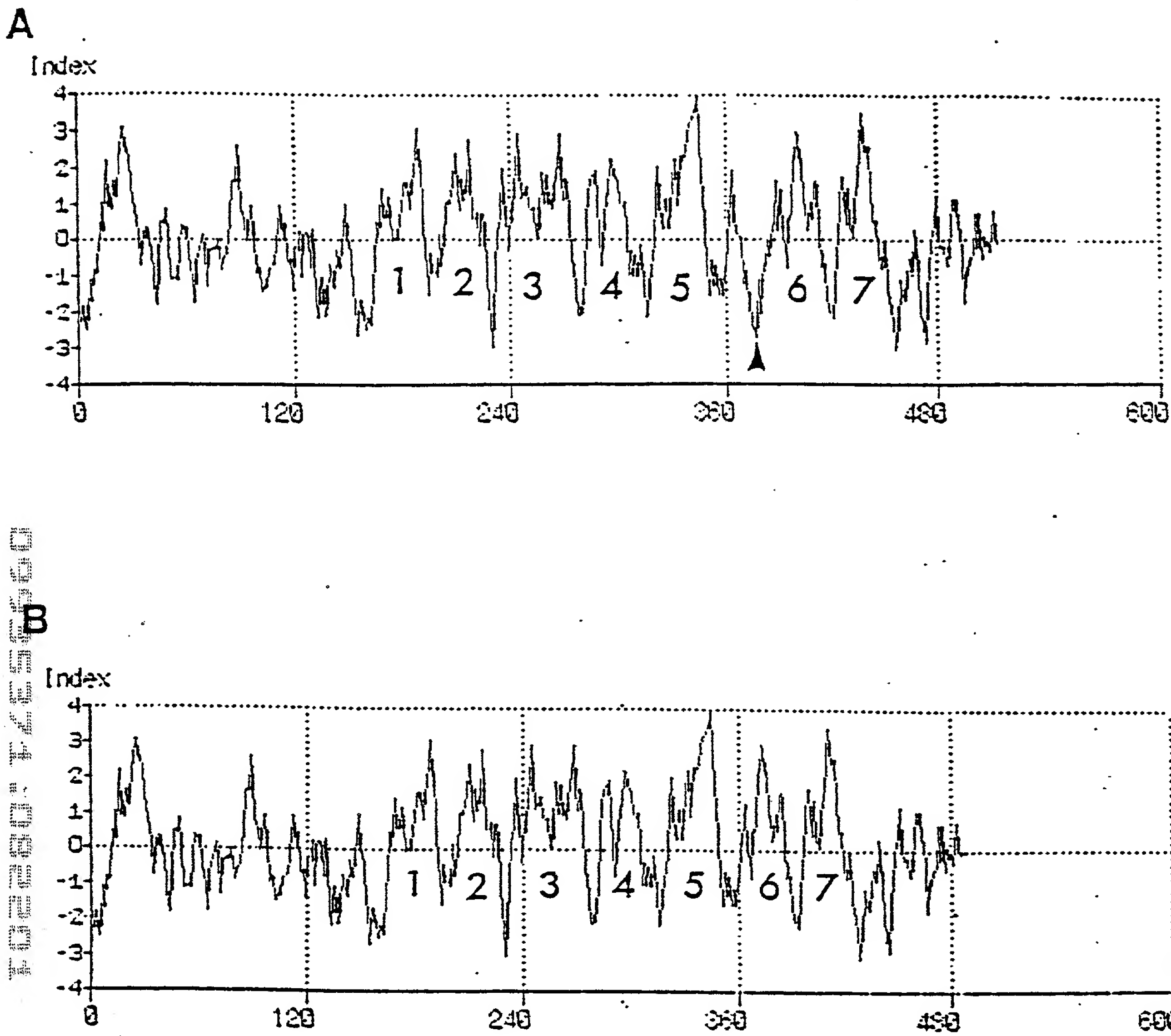
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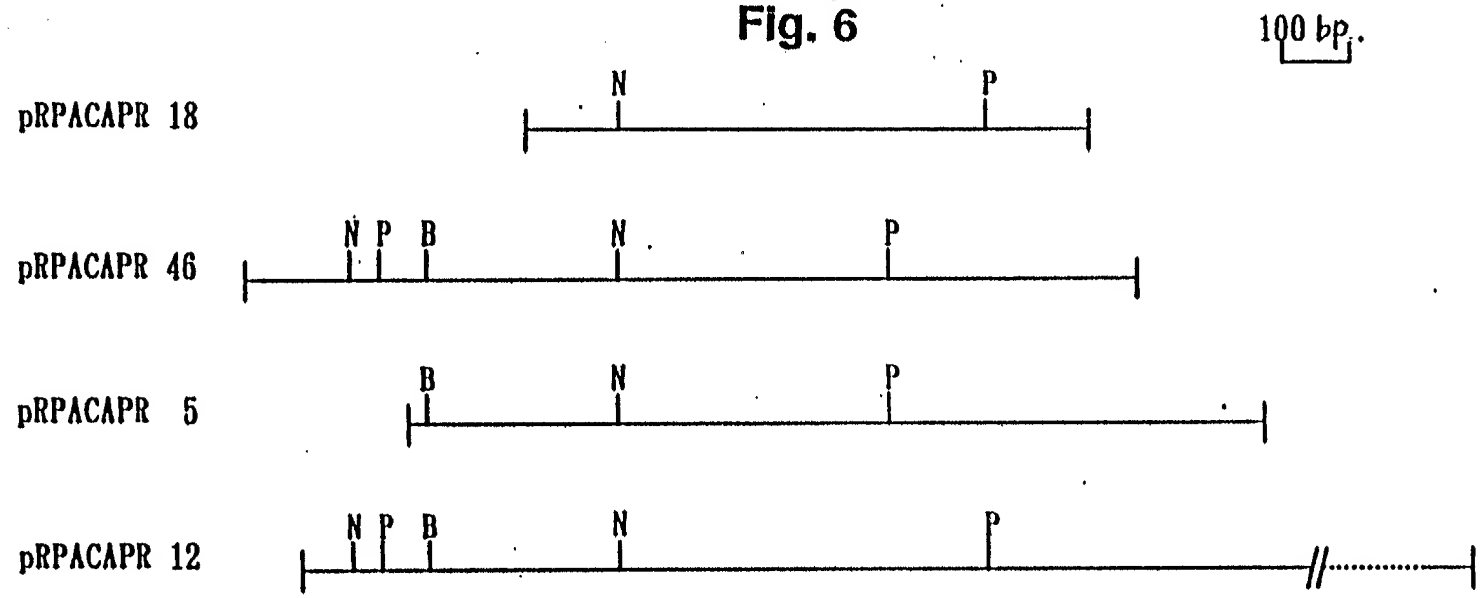
Fig. 6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pRPACAPR 46
N P B
N
P
pRPACAPR 5
B
N
P
pRPACAPR 12
N P B
N
P

Fig. 7

1 CGAGTGGACAGTGGCAGGCGGTGACTGAATCTCCAAGTCTGGAAACAATAGCCAGAGA 58

59 TAGTGGCTGGGAAGCACCATGGCCAGAGTCCTGCAGCTCTCCCTGACTGCTCTCCTGCTG 118
1 MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu 14

119 CCTGTGGCTATTGCTATGCACTCTGACTGCATCTTCAAGAAGGAGCAAGCCATGTGCCTG 178
15 ProValAlaIleAlaMetHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu 34

179 GAGAGGATCCAGAGGGCCAACGACCTGATGGGACTAAACGAGTCTTCCCCAGGTTGCCCT 238
35 GluArgIleGlnArgAlaAsnAspLeuMetGlyLeuAsnGluSerSerProGlyCysPro 54

239 GGCATGTGGGACAATATCACATGTTGGAAGCCAGCTCAAGTAGGTGAGATGGTCCTTGTA 298
55 GlyMetTrpAspAsnIleThrCysTrpLysProAlaGlnValGlyGluMetValLeuVal 74

299 AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA 358
75 SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle 94

359 GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGGAGATCACAGACATGGGGGTCGTGGGC 418
95 GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly 114

419 CGGAACTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG 478
115 ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly 134

479 TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT 538
135 PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla 154

539 CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG 598
155 LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu 174

599 TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC 658
175 CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer 194

659 TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC 718
195 PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp 214

719 AGCAGTCACTGCTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC 778
215 SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr 234

779 TGCGTGGTGTCCAACTACTTCTGGCTGTTCATTGAAGGCCTGTACCTCTTTACACTGCTG 838
235 CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu 254

839 GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG 898
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899 ACACCTACTGTGTGTGTAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA 958
275 ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly 294

959 TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCCGTGGTTGGC 1018
295 CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly 314

1019 TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCATCCTTGTACAGAAGCTG 1078
315 SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu 334

1079 CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTACGGCTGGCCCGCTCCACC 1138
335 GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrLeuArgLeuAlaArgSerThr 354

Fig. 8

```
1139 CTACTGCTCATCCCACTCTTCGGAATCCACTACACAGTATTCGCCTTCTCTCCAGAGAAC 1198
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1199 GTCAGCAAGAGGGAAAGACTTGTGTTTGAGCTTGGGCTGGGCTCCTTCCAGGGCTTTGTG 1258
 375 ValSerLysArgGluArgLeuValPheGluLeuGlyLeuGlySerPheGlnGlyPheVal  394

1259 GTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTACAGGCAGAGATTAAGAGGAAATGG 1318
 395 ValAlaValLeuTyrCysPheLeuAsnGlyGluValGlnAlaGluIleLysArgLysTrp  414

1319 AGGAGCTGGAAGGTGAACCGTTACTTCACTATGGACTTCAAGCACCGGCACCCGTCCCTG 1378
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1499 TTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAGCATGTTTGTGCCTCTCCCCTCTCC 1558
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1859 GGGGTAGTGCC                                                  1869
```

Fig. 9

1 CGAGTGGACAGTGGCAGGCGGTGACTGAATCTCCAAGTCTGGAAACAATAGCCAGAGA 58

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1 MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu 14

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15 ProValAlaIleAlaMetHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu 34

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35 GluArgIleGlnArgAlaAsnAspLeuMetGlyLeuAsnGluSerSerProGlyCysPro 54

239 GGCATGTGGGACAATATCACATGTTGGAAGCCAGCTCAAGTAGGTGAGATGGTCCTTGTA 298
55 GlyMetTrpAspAsnIleThrCysTrpLysProAlaGlnValGlyGluMetValLeuVal 74

299 AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA 358
75 SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle 94

359 GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGGAGATCACAGACATGGGGGTCGTGGGC 418
95 GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly 114

419 CGGAACTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG 478
115 ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly 134

479 TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT 538
135 PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla 154

539 CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG 598
155 LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu 174

599 TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC 658
175 CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer 194

659 TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC 718
195 PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp 214

719 AGCAGTCACTGCTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC 778
215 SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr 234

779 TGCGTGGTGTCCAACTACTTCTGGCTGTTCATTGAAGGCCTGTACCTCTTTACACTGCTG 838
235 CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu 254

839 GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG 898
255 ValGluThrPhePheProGluArgArgTyrPheTyrTrpTyrThrIleIleGlyTrpGly 274

899 ACACCTACTGTGTGTGTAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA 958
275 ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly 294

959 TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCCGTGGTTGGC 1018
295 CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly 314

1019 TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCATCCTTGTACAGAAGCTG 1078
315 SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu 334

1079 CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTCAGCTGCGTGCAGAAATGC 1138
335 GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrPheSerCysValGlnLysCys 354

Fig. 10

```
1139 TACTGCAAGCCACAGCGGGCTCAGCAGCACTCTTGCAAGATGTCAGAACTATCCACCATT 1198
 355 TyrCysLysProGlnArgAlaGlnGlnHisSerCysLysMetSerGluLeuSerThrIle  374

1199 ACTCTACGGCTGGCCCGCTCCACCCTACTGCTCATCCCACTCTTCGGAATCCACTACACA 1258
 375 ThrLeuArgLeuAlaArgSerThrLeuLeuLeuIleProLeuPheGlyIleHisTyrThr  394

1259 GTATTCGCCTTCTCTCCAGAGAACGTCAGCAAGAGGGAAAGACTTGTGTTTGAGCTTGGG 1318
 395 ValPheAlaPheSerProGluAsnValSerLysArgGluArgLeuValPheGluLeuGly  414

1319 CTGGGCTCCTTCCAGGGCTTTGTGGTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTA 1378
 415 LeuGlySerPheGlnGlyPheValValAlaValLeuTyrCysPheLeuAsnGlyGluVal  434

1379 CAGGCAGAGATTAAGAGGAAATGGAGGAGCTGGAAGGTGAACCGTTACTTCACTATGGAC 1438
 435 GlnAlaGluIleLysArgLysTrpArgSerTrpLysValAsnArgTyrPheThrMetAsp  454

1439 TTCAAGCACCGGCACCCGTCCCTGGCCAGCAGTGGAGTAAATGGGGGAACCCAGCTGTCC 1498
 455 PheLysHisArgHisProSerLeuAlaSerSerGlyValAsnGlyGlyThrGlnLeuSer  474

1499 ATCCTGAGCAAGAGCAGCTCCCAGCTCCGCATGTCCAGCCTCCCGGCCGACAACTTGGCC 1558
 475 IleLeuSerLysSerSerSerGlnLeuArgMetSerSerLeuProAlaAspAsnLeuAla  494

1559 ACCTGAGGCCTGTCTCCCTCCTCCTTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAG 1618
 495 Thr***                                                        495

1619 CATGTTTGTGCCTCTCCCCTCTCCTTGGGCAGGCCCTGGGTAGGAAGCTGGGCTCCTCCC 1678
1679 CAAAGGGGAAGAGAGAGATAGGGTATAGGCTGATATTGCTCCTCCTGTTTGGGTCCCACC 1738
1739 TACTGTGATTCATTGAGCCTGATTTGACATGTAAATACACCTCAAATTTGGAAAGTTGCC 1798
1799 CCATCTCTGCCCCCAACCCATGCCCCTGCTCACCTCTGCCAGGCCCCAGCTCAACCTACT 1858
1859 GTGTCAAGGCCAGCCTCAGTGATAGTCTGATCCCAGGTACAAGGCCTTGTGAGCTGAGGC 1918
1919 TGAAAGGCCTGTTTTGGAGAGGCTGGGGTAGTGCCCACCCCAGCAGCCTTTCAGCAAATT 1978
1979 GACTTTGGATGTGGACCCTTCTCAGCCTGTACCAAGTACTGCAGTTGGCTAGGGATGCAG 2038
2039 CTCAGTTTCCTGAGCATCCTTTGGAGCAGGTCAACCTGAGGCTCCTTTTGCTTACCCGAC 2098
2099 ATCTAAGTTGTCCAGGTGCTCGGCTCCTGTGTGCCTGGATGACGGGAGGGCTCCGGGGTC 2158
2159 TTTCAGTCAAAGACTTACATTGAGGTGGGGTGAGAGTCAGAGAAAAGTTCTGGTGCTTTT 2218
2219 CATTTGTTCTAAGAGCTGAGAGCCAGGAATGCAGAGTCAATTGGGAAGGAGATGGGATAG 2278
2279 CTGATGATCTTACCATGTCCATGACTGTGCCCCTGATTCAAGACCGGATCATGTGGTGGC 2338
2339 TTTATTTCTACACTTCTTGTCCACAATGGACAGTCTGAGGAAGCTCTTCTTTCAGCCACA 2398
2399 ACAACCACAGAAAGCCCTTTCTTCTCCCCTCTTGTTTCTCCATAAGTCAAAGCCATGTTT 2458
2459 AGAACGGACCAGCCACCTTGCGATGAAATCACTGAGTTCTGAAGCAACTTTCAATTTCCA 2518
2519 CGAGCCAAGTCCTGGTCCAGGACGCCCC                                 2548
```

Fig. 11

Rat	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	1				5					10					15	

Rat	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu
		*	*	*		*	*	*	*	*	*	*	
Bovine	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp
				20					25				

Fig. 12

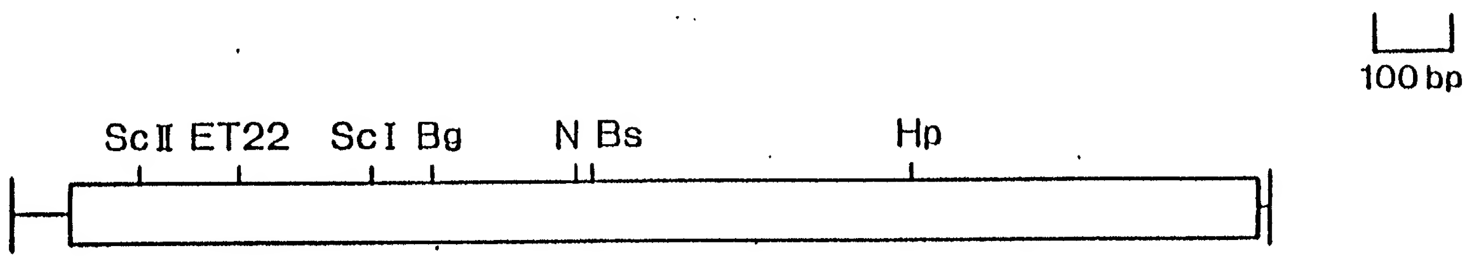

Fig. 13

1	AGCCCAGAGACACATTGGGGCTGACCTGCCGCTGCTGTCAGTGGGAGGCCAGTGGTGCTGGCCAAGAAGTGTC ATG	76
1	Met	1
77	GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC	136
2	Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly	21
137	AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC	196
22	Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp	41
197	CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC	256
42	Leu Pro Leu Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val	61
257	GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC	316
62	Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp	81
317	TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG	376
82	Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu	101
377	ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG	436
102	Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp	121
437	AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC TTC	496
122	Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe	141
497	AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC AGT AAC	556
142	Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser Asn	161
557	TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG	616
162	Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser	181
617	GAA CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG	676
182	Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly	201
677	GAC CAG GAT TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC	736
202	Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser	221
737	CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA	796
222	Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr	241
797	CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC	856
242	Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe	261
857	ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG	916
262	Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val	281
917	GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG CTG	976
282	Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu	301
977	TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG AGA	1036
302	Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg	321
1037	TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG	1096
322	Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp	341
1097	GCT ACG CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT	1156
342	Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala	361
1157	CTG TGG TGG GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT	1216
362	Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe	381
1217	ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG	1276
382	Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu	401
1277	TCC AGC ATC TAC TTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC	1336
402	Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile	421
1337	CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT	1396
422	His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe	441
1397	GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT	1456
442	Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn	461
1457	GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC TTC	1516
462	Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe	481
1517	GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG GGC ACC	1576
482	Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr	501
1577	CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC	1636
502	Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp	521
1637	AAT CTG GCC ACC TGA GCCATGCTCCCCT	1664

Fig. 14

					5					10					15
Human	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu

					20					25				
Human	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp
	*	*	*	*	*		*		*	*	*		*	*
Bovine	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp

Fig. 15

Rat	Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
TypeI−B	AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG
pHPR15A	Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
humanTypeI−B	AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG
pHPR55A	Asn Glu Ser Ser Ile Tyr Phe — Cys Val Gln Lys Cys Tyr Cys Lys
TypeI−B2	AAT GAG TCC AGC ATC TAC TTC TGC GTG CAG AAA TGC TAC TGC AAG
pHPR66P	Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg Val Pro Lys
TypeI−C	AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA GTC CCC AAG

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTA TCC ACC
Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC
Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC
Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu
AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTA CGG CTG GCC CGC TCC ACC CTA
Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG
Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG
Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu
CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG

Fig. 16

1 A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA 67

1 Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly 21
68 AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC 136

22 Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu 44
137 AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG 205

45 Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala 67
206 CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT 274

68 Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met 90
275 GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG 343

91 Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly 113
344 TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG 412

114 Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu 136
413 ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG 481

137 Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp 159
482 CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC 550

160 Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu 182
551 AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA 619

183 Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr 205
620 CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT 688

206 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala 228
689 TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC 757

229 Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val 251
758 ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG 826

252 Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn 274
827 TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC 895

275 His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn 297
896 CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC 964

298 Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg 320
965 TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG 1033

321 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr 343
1034 AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG 1102

344 Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile 366
1103 CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC 1171

367 Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val 389
1172 AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG 1240

390 Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys 412
1241 CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC 1309

413 Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg 435
1310 TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTG CGA 1378

436 Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro 458
1379 CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA 1447

459 Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val 481
1448 GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG 1516

482 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys 504
1517 GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG 1585

505 Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly 527
1586 GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG 1654

528 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn 550
1655 GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT 1723

551 Leu Ala Thr *** 553
1724 CTG GCC ACC TGA GCC ATG CTC CCC T 1748

Fig. 17

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1     A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA      67

1             Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly      21
68     AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC     136

22     Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu     44
137    AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG     205

45     Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala     67
206    CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT     274

68     Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met     90
275    GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG     343

91     Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly     113
344    TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG     412

114    Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu     136
413    ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG     481

137    Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp     159
482    CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC     550

160    Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu     182
551    AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA     619

183    Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr     205
620    CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT     688

206    Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala     228
689    TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC     757

229    Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val     251
758    ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG     826

252    Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn     274
827    TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC     895

275    His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn     297
896    CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC     964

298    Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg     320
965    TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG     1033

321    Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr     343
1034   AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG     1102

344    Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile     366
1103   CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC     1171

367    Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val     389
1172   AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG     1240

390    Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr     412
1241   CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC TGC GTG CAG AAA TGC TAC     1309

413    Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu     435
1310   TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTG CGA CTG     1378

436    Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu     458
1379   GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG     1447

459    Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala     481
1448   AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT     1516

482    Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val     504
1517   GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG     1585

505    Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly     527
1586   AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG GGC     1654

528    Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu     550
1655   ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG     1723

                                                                                                  552
551    Ala Thr ***                                                                                1745
1724   GCC ACC TGA GCC ATG CTC CCC T
```

Fig. 18

```
1     A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA     67

1             Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly     21
68    AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC     136

22    Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu     44
137   AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG     205

45    Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala     67
206   CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT     274

68    Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met     90
275   GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG     343

91    Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly     113
344   TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG     412

114   Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu     136
413   ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG     481

137   Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp     159
482   CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC     550

160   Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu     182
551   AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA     619

183   Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr     205
620   CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT     688

206   Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala     228
689   TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC     757

229   Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val     251
758   ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG     826

252   Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn     274
827   TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC     895

275   His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn     297
896   CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC     964

298   Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg     320
965   TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG     1033

321   Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr     343
1034  AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG     1102

344   Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile     366
1103  CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC     1171

367   Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val     389
1172  AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG     1240

390   Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg     412
1241  CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA     1309

413   Val Pro Lys Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu Pro Phe Leu Arg     435
1310  GTC CCC AAG AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC CCT TTC CTG CGA     1378

436   Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro     458
1379  CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA     1447

459   Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val     481
1448  GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG     1516

482   Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys     504
1517  GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG     1585

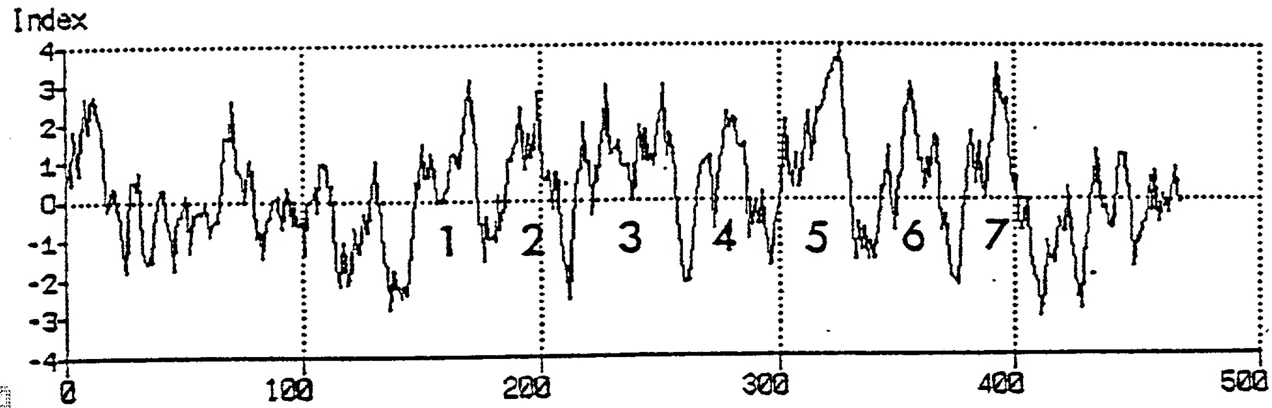
505   Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly     527
1586  GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG     1654

528   Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn     550
1655  GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT     1723

551   Leu Ala Thr ***                                                                                 553
1724  CTG GCC ACC TGA GCC ATG CTC CCC T                                                                1748
```

Fig. 19

A


Index
4
3
2
1
0
-1
-2
-3
-4
0
100
200
300
400
500
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2
3
4
5
6
7

B

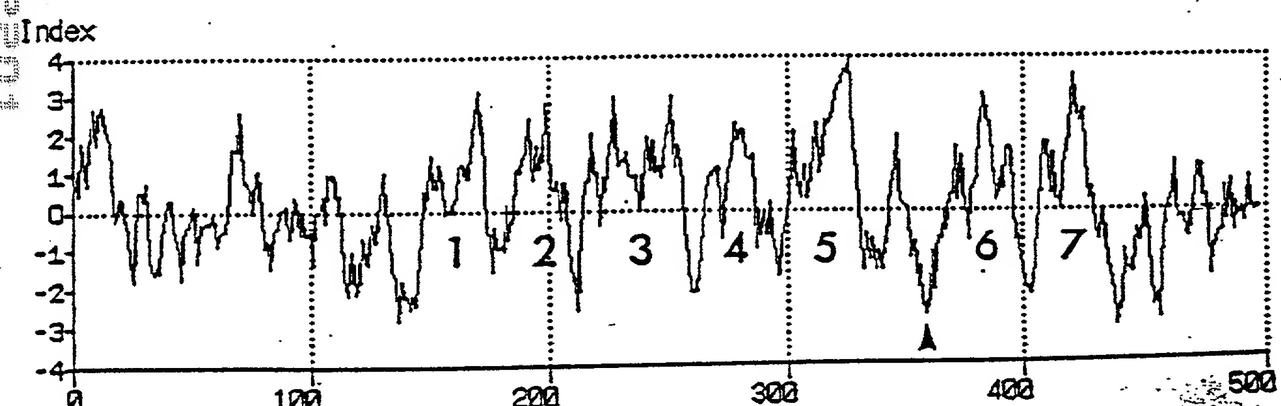
Index
4
3
2
1
0
-1
-2
-3
-4
0
100
200
300
400
500
1
2
3
4
5
6
7

Fig. 20

```
EQUIVALENT
   1 : Ala(A),Ser(S),Thr(T),Pro(P),Gly(G)
   2 : Asn(N),Asp(D),Asx(B),Glu(E),Gln(Q),Glx(Z)
   3 : His(H),Arg(R),Lys(K)
   4 : Met(M),Leu(L),Ile(I),Val(V)
   5 : Phe(F),Tyr(Y),Trp(W)

PACAP receptor (upper lines)

VIP   receptor (lower lines)

       19        29        39        49        59        69        79
TALLLPVAIAMHSDCIFKKEQAMCLERIQRANDLMGLNESSPGCPGMWDNITCWKPAQVGEMVLVSCPEV
     *  *          **    * *      *        * *     * *      **
MRPPSPPHVRWLCVLAGALACALRPAGSQAASPQHECEYLQLIEIQRQQCLEEAQLENETTGCSKMWDNL
       10        20        30        40        50        60        70

       89        99       109       119       129       139       149
FRIFNPDQVWMTETIGDSGFADSNSLEITDMGVVGRNCTEDGWSEPFPHYFDACGFDDYEPESGDQDYYY
     *              *     **   ***    * *      *  *   *        *  **  **
TCWPTTPRGQAVVLDCPLIFQLFAPIHGYNISRSCTEEGWSQLEPGPYHIACGLNDRASSLDEQQQTKFY
       80        90       100       110       120       130       140

      159       169       179       189       199       209       219
LSVKALYTVGYSTSLATLTTAMVILCRFRKLHCTRNFIHMNLFVSFMLRAISVFIKDWILYAEQDSSHCF
 **** ****** *****  ** **  ************* ********* ******   **   *  **
NTVKTGYTIGYSLSLASLLVAMAILSLFRKLHCTRNYIHMHLFMSFILRATAVFIKDMALFNSGEIDHCS
      150       160       170       180       190       200       210

      229       239       249       259       269       279       289
VSTVECKAVMVFFHYCVVSNYFWLFIEGLYLFTLLVETFFPERRYFYWYTIIGWGTPTVCVTVWAVLRLY
 *** *** **** *********** **********  *********** * ***** *** **********
EASVGCKAAVVFFQYCVMANFFWLLVEGLYLYTLLAVSFFSERKYFWGYILIGWGVPSVFITIWTVVRIY
      220       230       240       250       260       270       280

      299       309       319       329       339       349       359
FDDAGCWDMNDSTALWWVIKGPVVGSIMVNFVLFIGIIIILVQKLQSPDMGGNESSIYLRLARSTLLLIP
*** ****    ************ ********** ** ****** ***** **** * ***********
FEDFGCWDTIINSSLWWIIKAPILLSILVNFVLFICIIRILVQKLRPPDIGKNDSSPYSRLAKSTLLLIP
      290       300       310       320       330       340       350

      369       379       389       399       409       419       429
LFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVVAVLYCFLNGEVQAEIKRKWRSWKVNRYFTMDFKH
****** **** ***      ****** ***************************** ****    *   *
LFGIHYVMFAFFPDNFKAQVKMVFELVVGSFQGFVVAILYCFLNGEVQAELRRKWRRWHLQGVLGWSSKS
      360       370       380       390       400       410       420

      439       449       459
RHPSLASSGVNGGTQLSILSKSSSQLRMSSLPADNLAT*
 **  ** *   ********** **  * **    ***
QHPWGGSNGATCSTQVSMLTRVSPSARRSSSFQAEVSLV
      430       440       450
```

Fig. 21

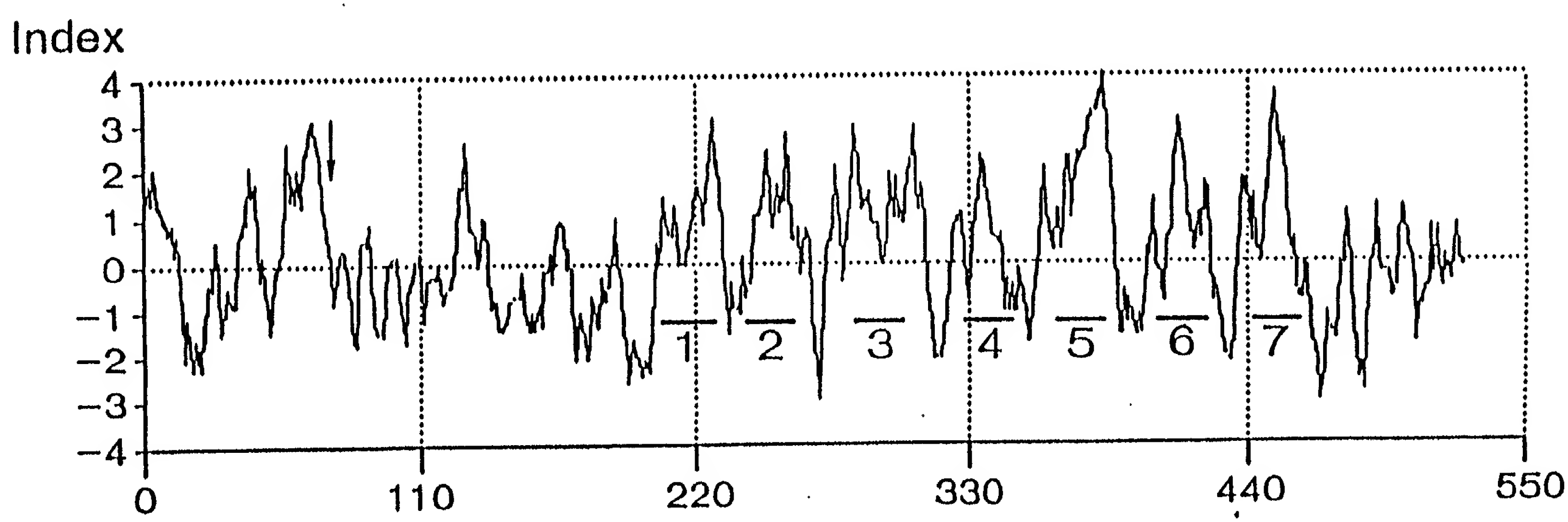

Fig. 22

```
                10         20         30         40         50         60         70         80
HUMAN   MAGVVHVSLA AHCGACPWGR GRLRKGRAAC KSAAQRHIGA DLPLLSVGGQ WCWPRSVMAG VVHVSLAALL LLPMAPAMHS
BOVINE  .......... .......... .......... .......... MRGGRHWPEP PCRLRSVMAS IAQVSLAALL LLPMATAMHS
RAT     .......... .......... .......... .......... .......... .......MAR VLQLSLTALL L-PVAIAMHS

                90        100        110        120        130        140        150        160
        DCIFKKEQAM CLEKIQRANE LMGFNDSSPG CPGMWDNITC WKPAHVGEMV LVSCPELFRI FNPDQVWETE TIGESDFGDS
        DCIFKKEQAM CLEKIQRVND LMGLNDSSPG CPGMWDNITC WKPAHVGEMV LVSCPELFRI FNPDQVWETE TIGEFGFADS
        DCIFKKEQAM CLERIQRAND LMGLNESSPG CPGMWDNITC WKPAQVGEMV LVSCPEVFRI FNPDQVWMTE TIGDSGFADS

               170        180        190        200        210        220        230        240
        NSLDLSDMGV VSRNCTEDGW SEPFPHYFDA CGFDEYESET GDQDYYYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC
        KSLDLSDMRV VSRNCTEDGW SEPFPHYFDA CGFEEYESET GDQDYYYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC
        NSLEITDMGV VGRNCTEDGW SEPFPHYFDA CGFDDYEPES GDQDYYYLSV KALYTVGYST SLATLTTAMV ILCRFRKLHC

               250        260        270        280        290        300        310        320
        TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSNHCFIST VECKAVMVFF HYCVVSNYFW LFIEGLYLFT LLVETFFPER
        TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSNHCFVST VECKAVMVFF HYCVVSNYFW LFIEGLYLFT LLVETFFPER
        TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSSHCFVST VECKAVMVFF HYCVVSNYFW LFIEGLYLFT LLVETFFPER

               330        340        350        360        370        380        390        400
        RYFYWYTIIG WGTPTVCVTV WATLRLYFDD TGCWDMNDST ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGGN
        RYFYWYIIIG WGTPTVCVSV WAMLRLYFDD TGCWDMNDNT ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGGN
        RYFYWYTIIG WGTPTVCVTV WAVLRLYFDD AGCWDMNDST ALWWVIKGPV VGSIMVNFVL FIGIITILVQ KLQSPDMGGN

               410        420        430        440        450        460        470        480
        ESSIY----- ---------- ---------- ---LRLARST LLLIPLFGIH YTVFAFSPEN VSKRERLVFE LGLGSFQGFV
        ESSIYFSCVQ KCYCKPQRAQ QHSCKMSELS TITLRLARST LLLIPLFGIH YTVFAFSPEN VSKRERLVFE LGLGSFQGFV
        ESSIYFSCVQ KCYCKPQRAQ QHSCKMSELS TITLRLARST LLLIPLFGIH YTVFAFSPEN VSKRERLVFE LGLGSFQGFV

               490        500        510        520        530        540        550
        VAVLYCFLNG EVQAEIKRKW RSWKVNRYFA VDFKHRHPSL ASSGVNGGTQ LSILSKSSSQ IRMSGLPADN LAT
        VAVLYCFLNG EVQAEIKRKW RSWKVNRYFT MDFKHRHPSL ASSGVNGGTQ LSILSKSSSQ IRMSGLPADN LAT
        VAVLYCFLNG EVQAEIKRKW RSWKVNRYFT MDFKHRHPSL ASSGVNGGTQ LSILSKSSSQ LRMSSLPADN LAT
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Fig. 23

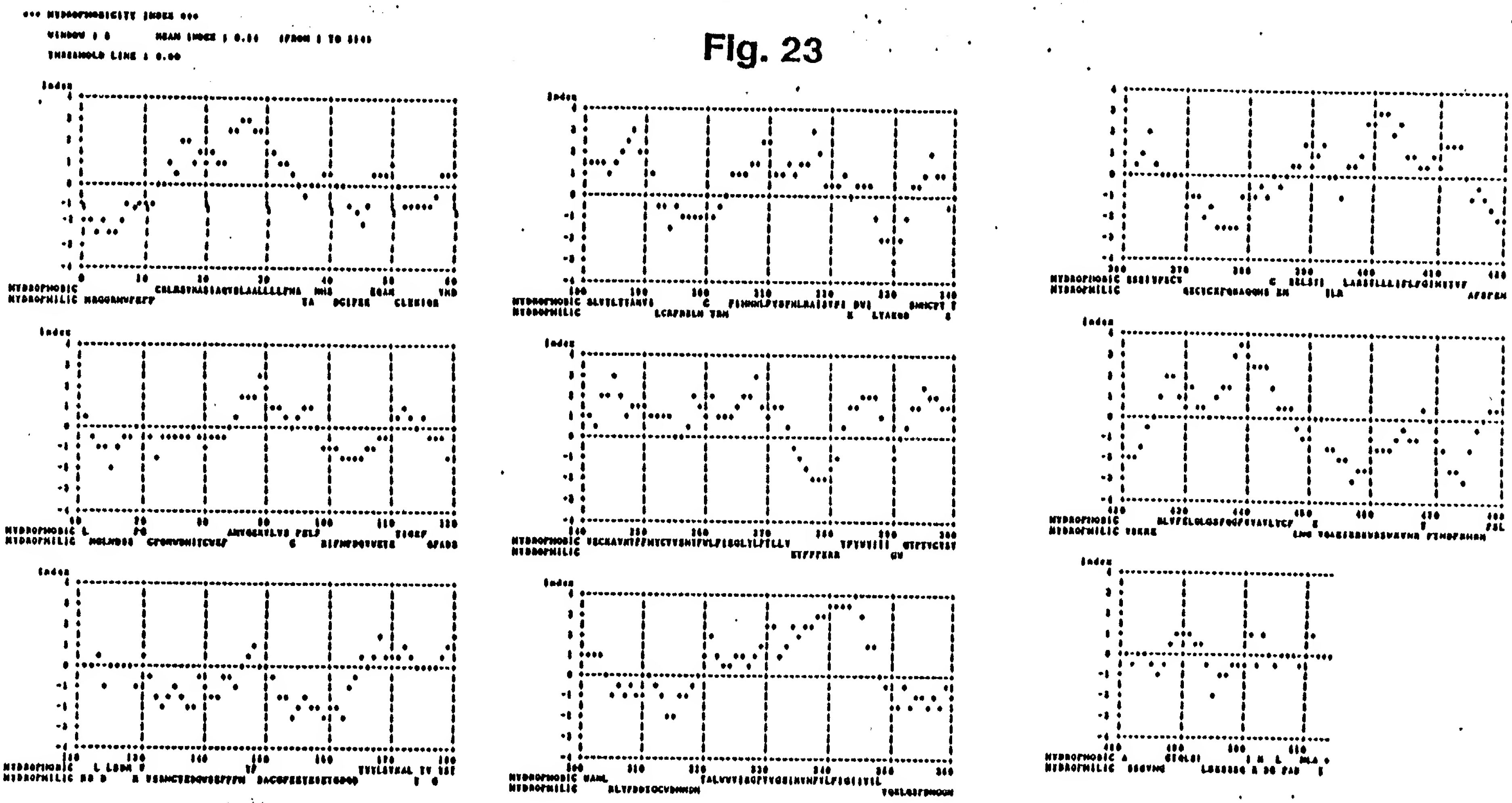
*** HYDROPHOBICITY INDEX ***
THRESHOLD LINE
HYDROPHOBIC
HYDROPHILIC

Fig. 24

DNASIS ***** HYDROPHOBICITY ANALYSIS LIST ***** DATE 92-10-19

*** INPUT INFORMATION ***

FILE NAME : DFAAO.AMI

HYDROPHOBICITY INDEX TABLE FILE : HYTE.THA

*** HYDROPHOBICITY INDEX ***

WINDOW : 6 MEAN INDEX : 0.10 (FROM 1 TO 466)

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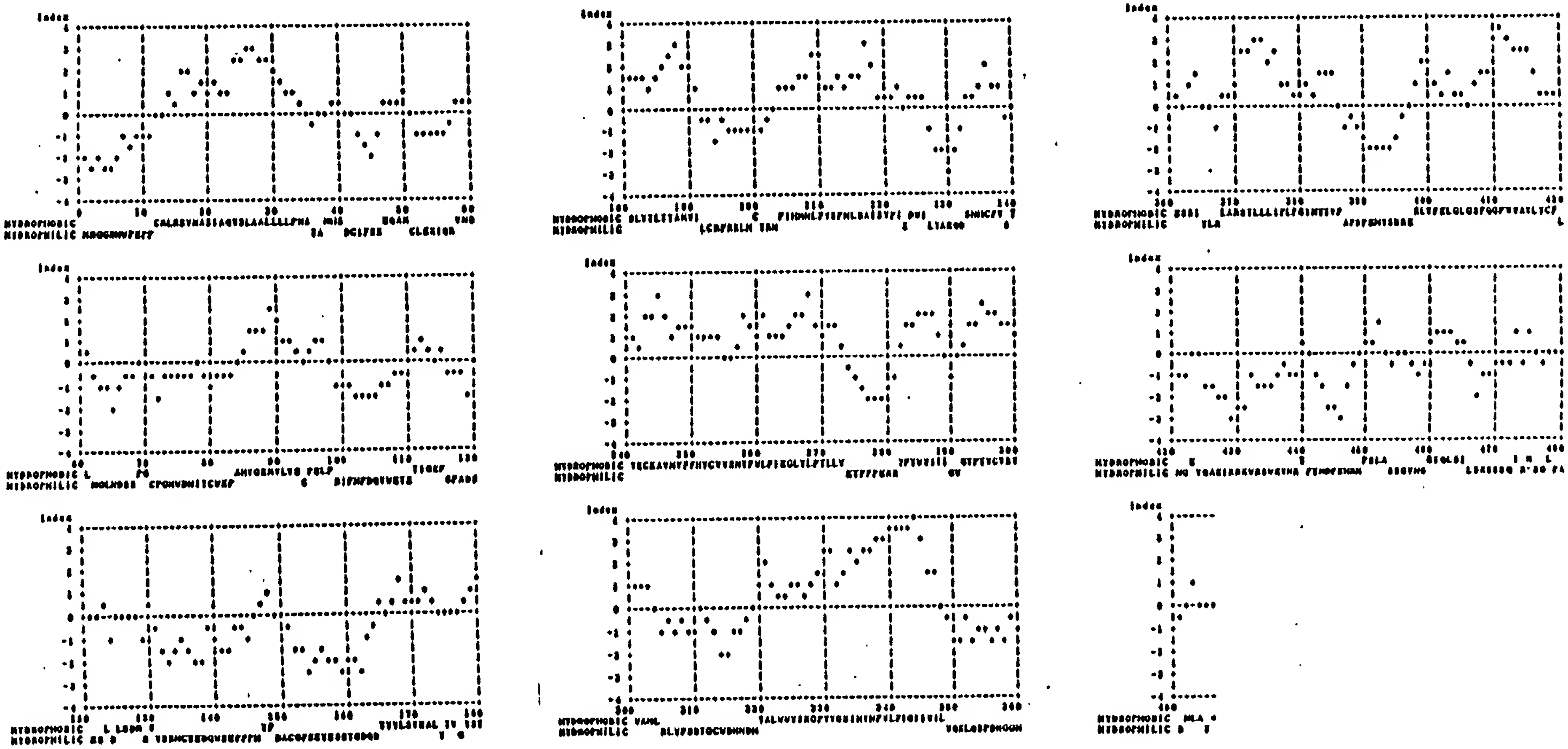


Fig. 25

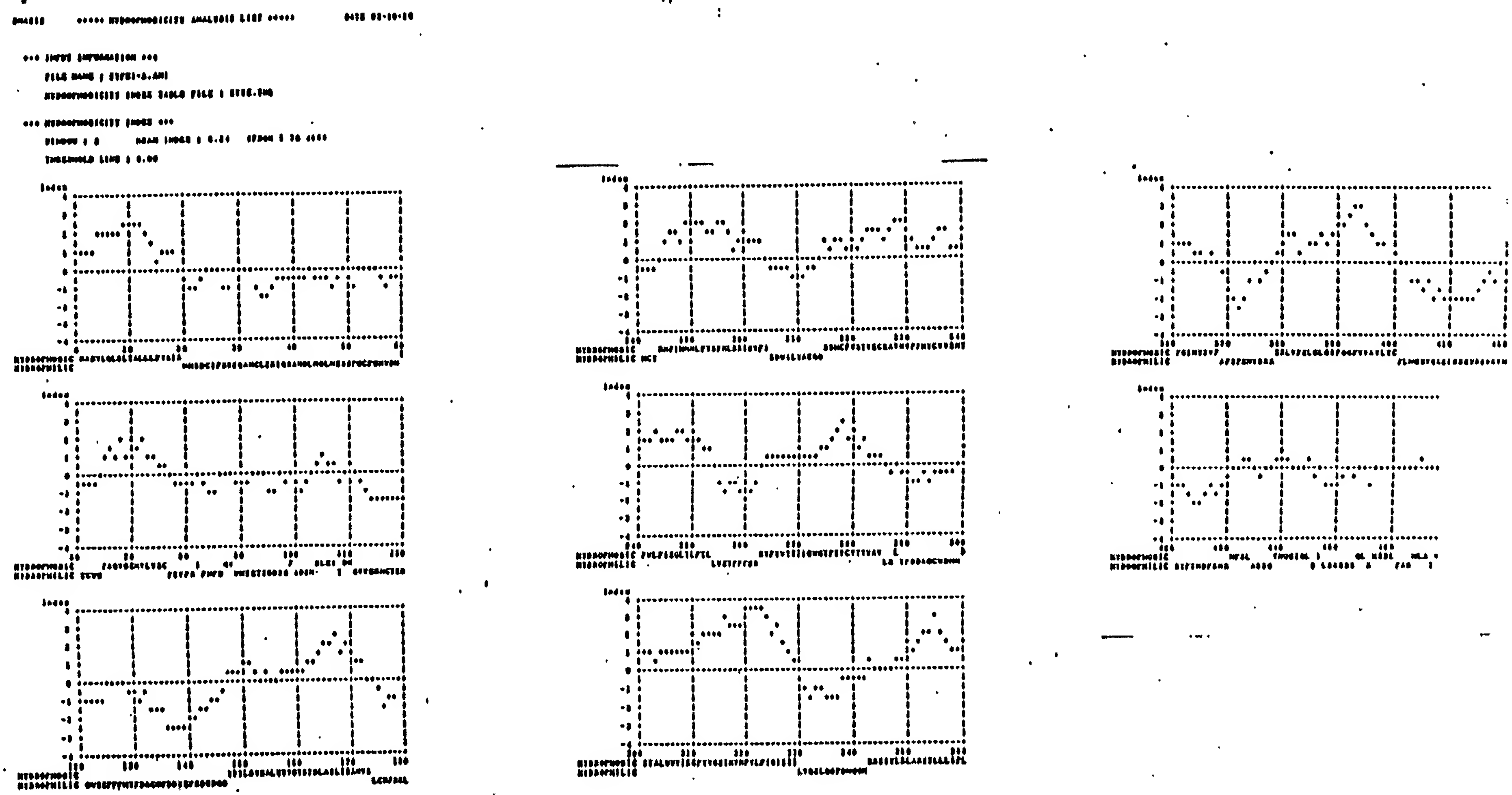


Fig. 26

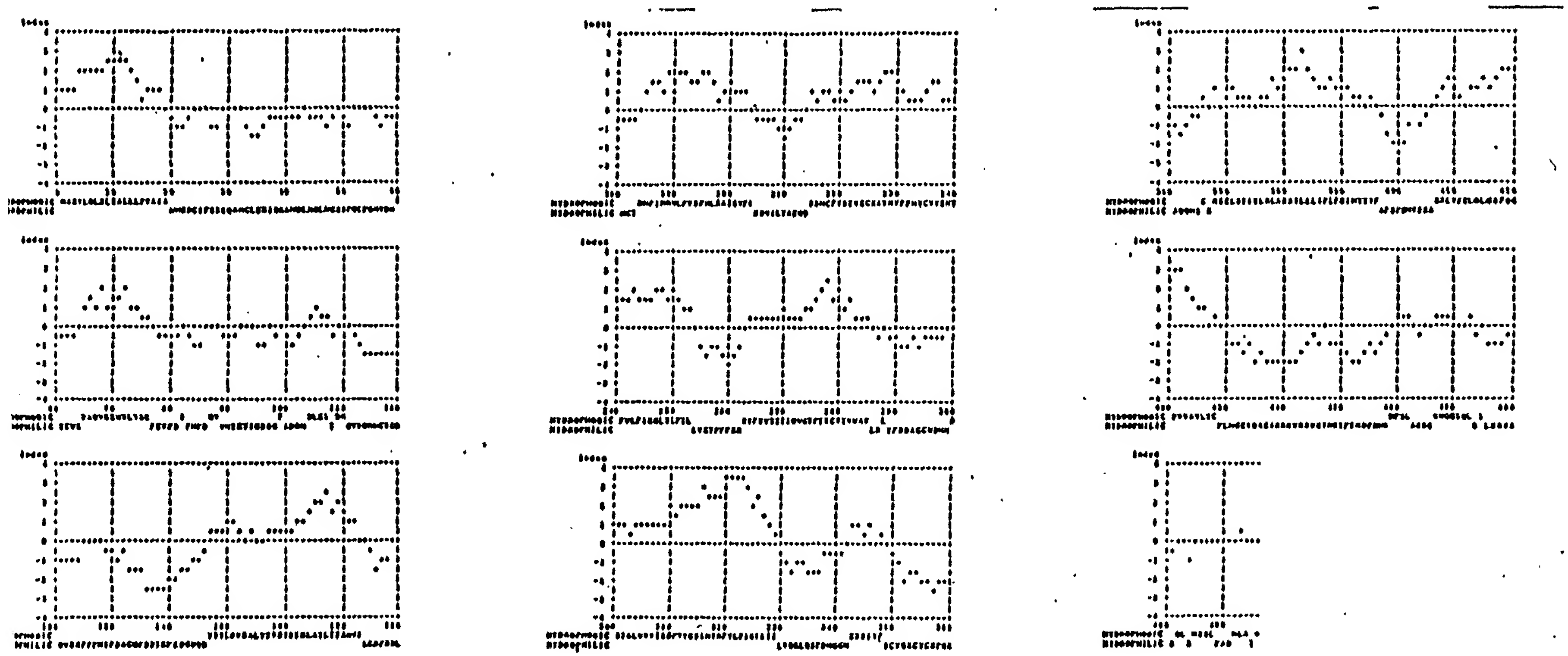


Fig. 27

[illegible] ***** HYDROPHOBICITY ANALYSIS LIST ***** DATE [illegible]

*** INPUT INFORMATION ***

FILE NAME : [illegible]

HYDROPHOBICITY INDEX TABLE FILE : [illegible]

*** HYDROPHOBICITY INDEX ***

WINDOW : [illegible] MEAN INDEX : [illegible] (FROM 1 TO [illegible])

THRESHOLD LINE : [illegible]

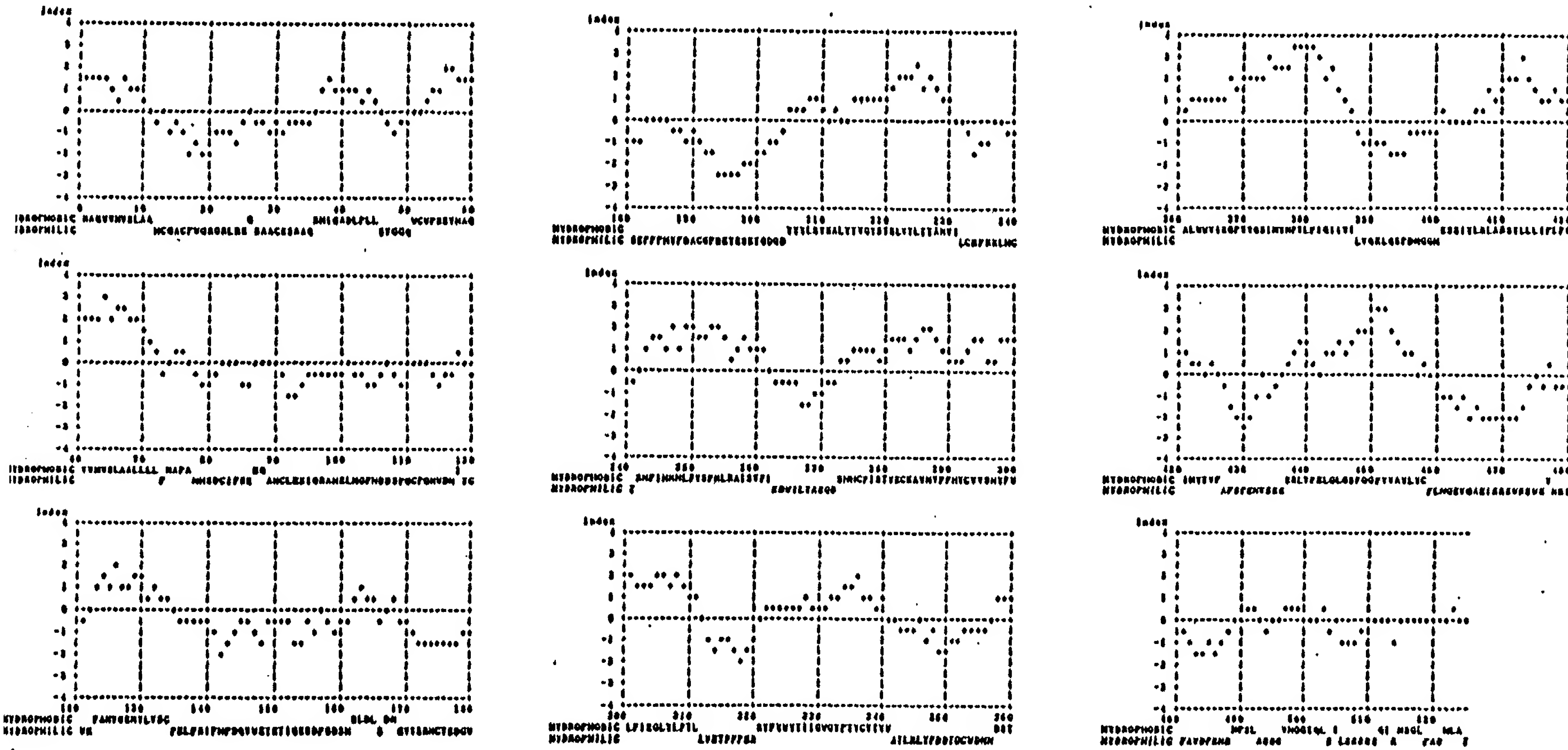


Fig. 28

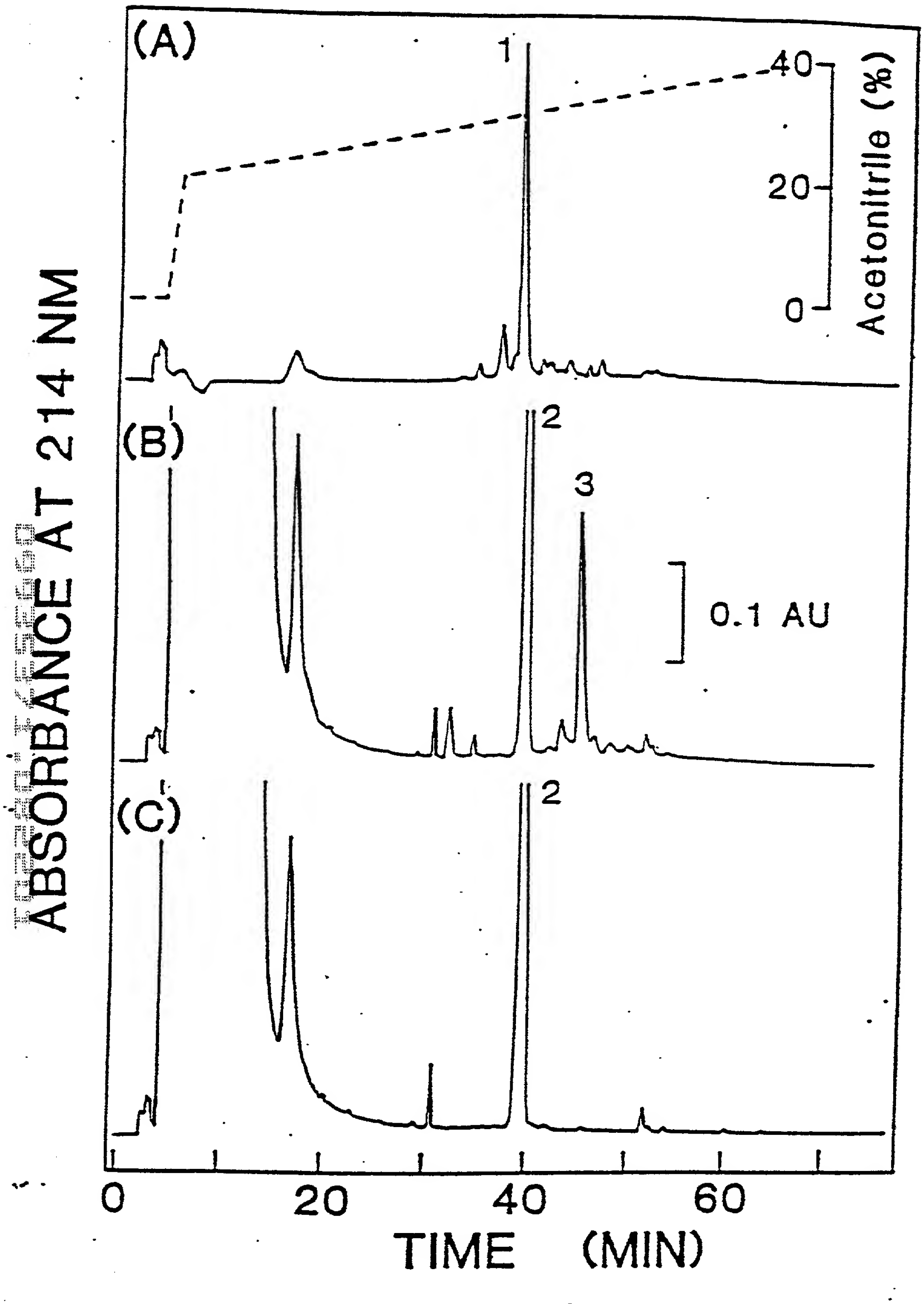

(A)
1
40
20
0
Acetonitrile (%)
(B)
2
3
0.1 AU
(C)
2
ABSORBANCE AT 214 NM
0
20
40
60
TIME (MIN)

Fig. 29

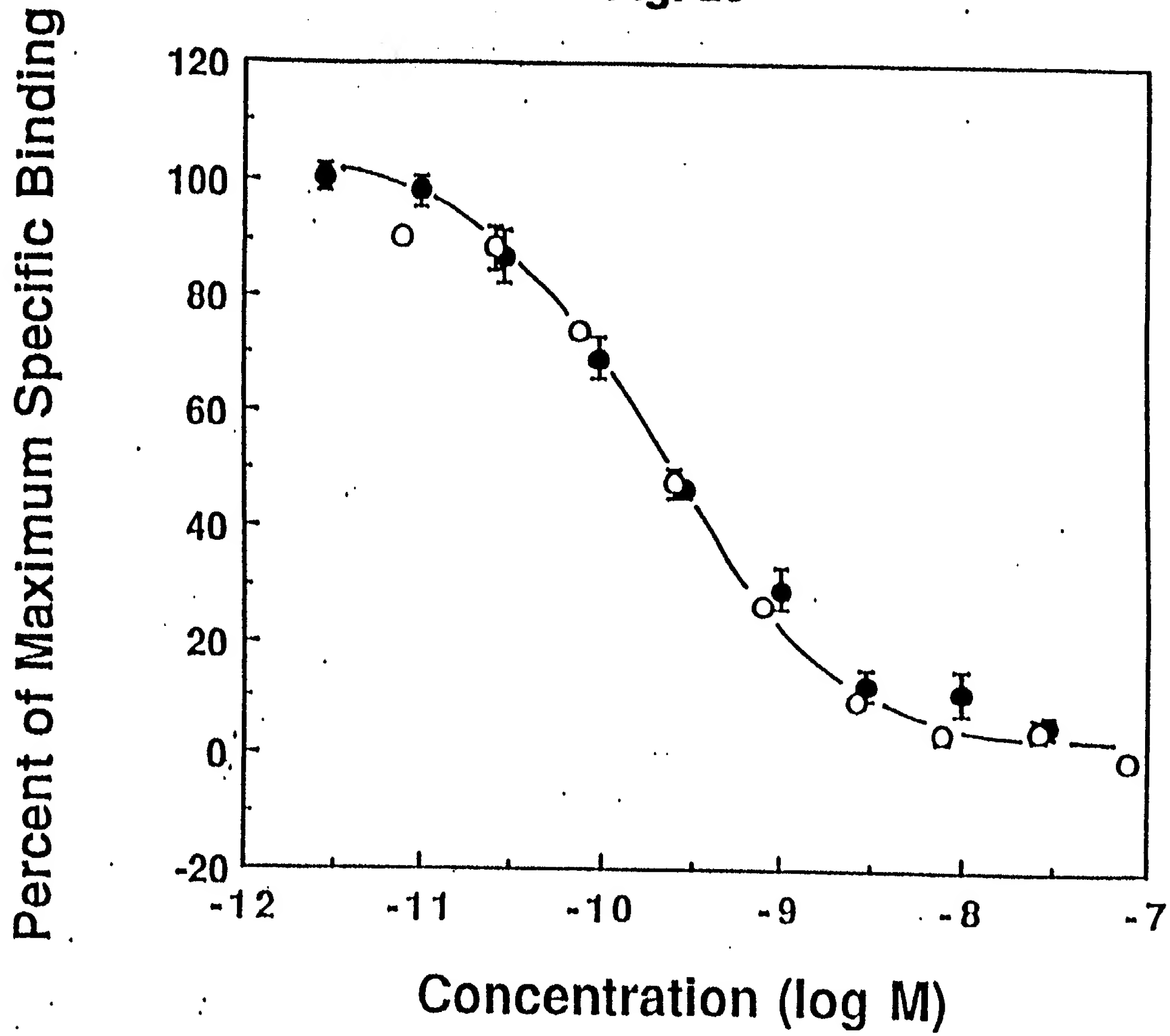

Percent of Maximum Specific Binding
120
100
80
60
40
20
0
-20
-12
-11
-10
-9
-8
-7
Concentration (log M)

Fig. 30

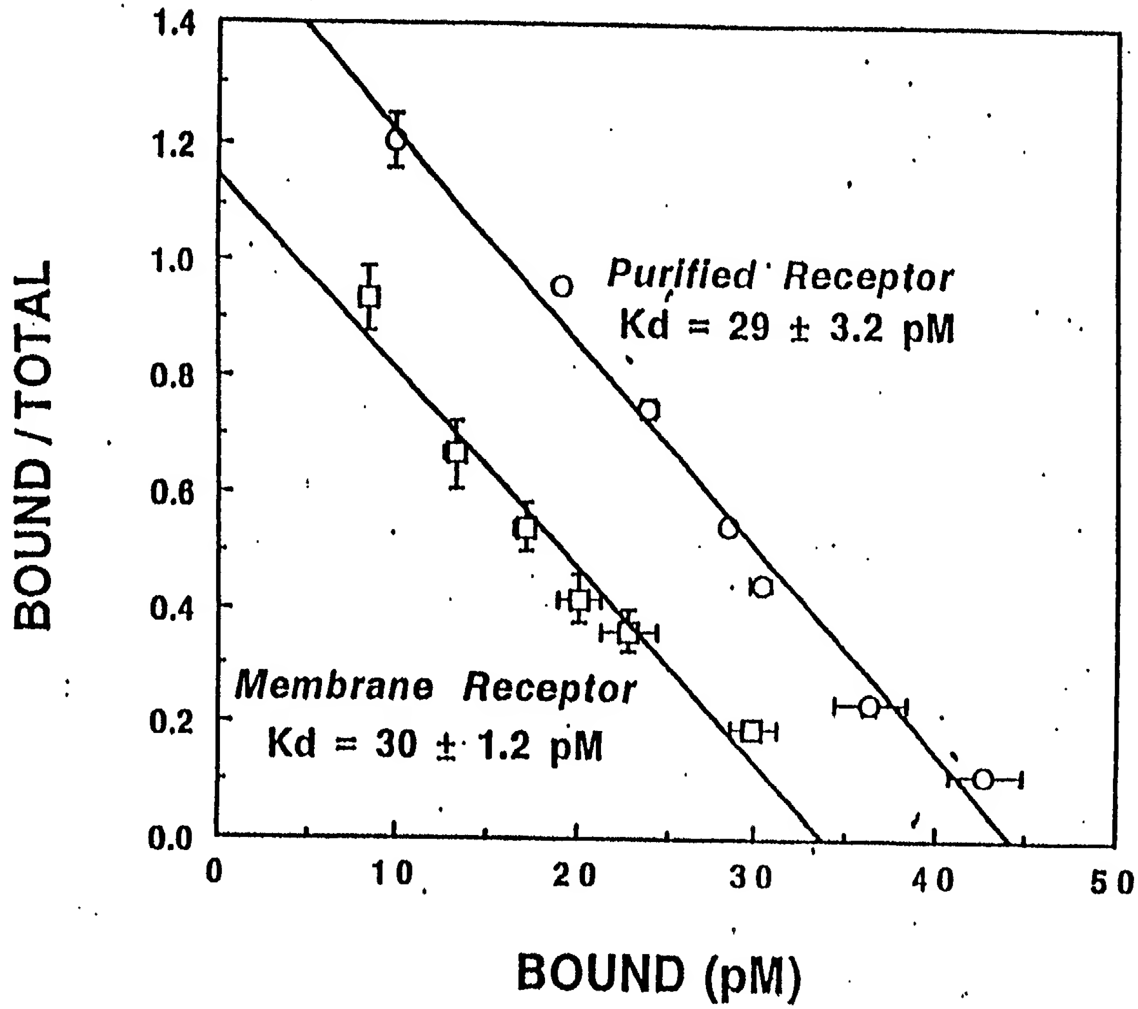
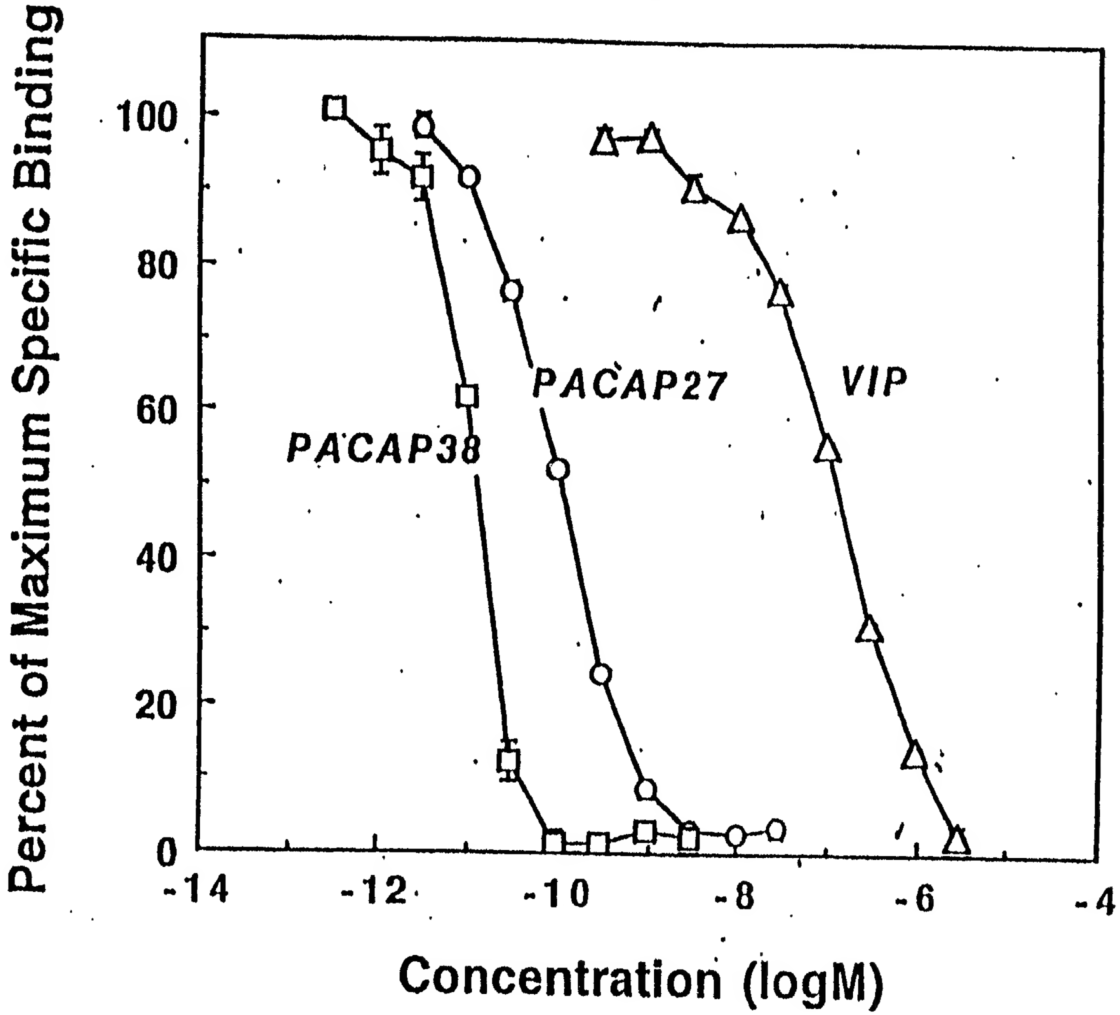

BOUND / TOTAL
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Purified Receptor
Kd = 29 ± 3.2 pM
Membrane Receptor
Kd = 30 ± 1.2 pM
0
10
20
30
40
50
BOUND (pM)

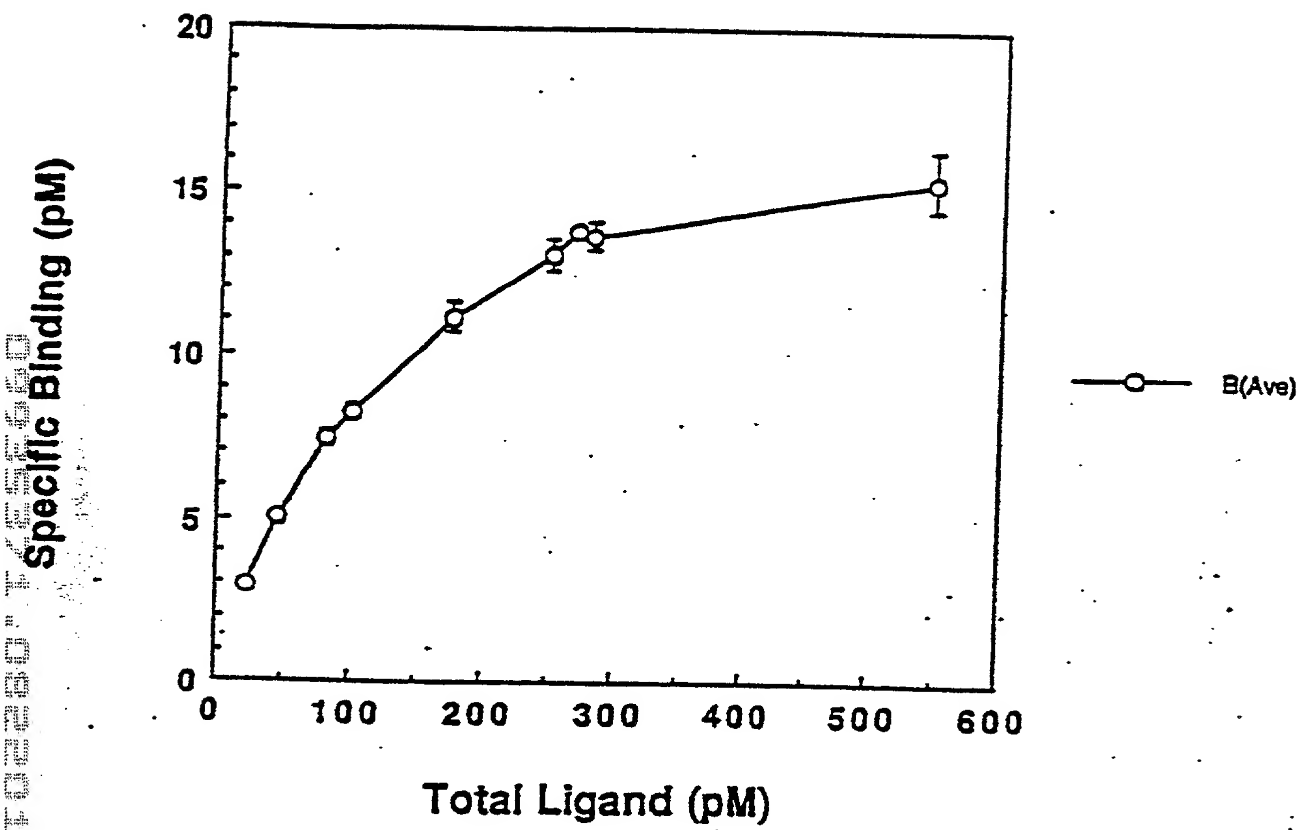
Fig. 31



Percent of Maximum Specific Binding
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
Concentration (logM)
PACAP38
PACAP27
VIP

Fig. 32

Fig. 33



Specific Binding (pM)
20
15
10
5
0
0
100
200
300
400
500
600
Total Ligand (pM)
B(Ave)

Fig. 34

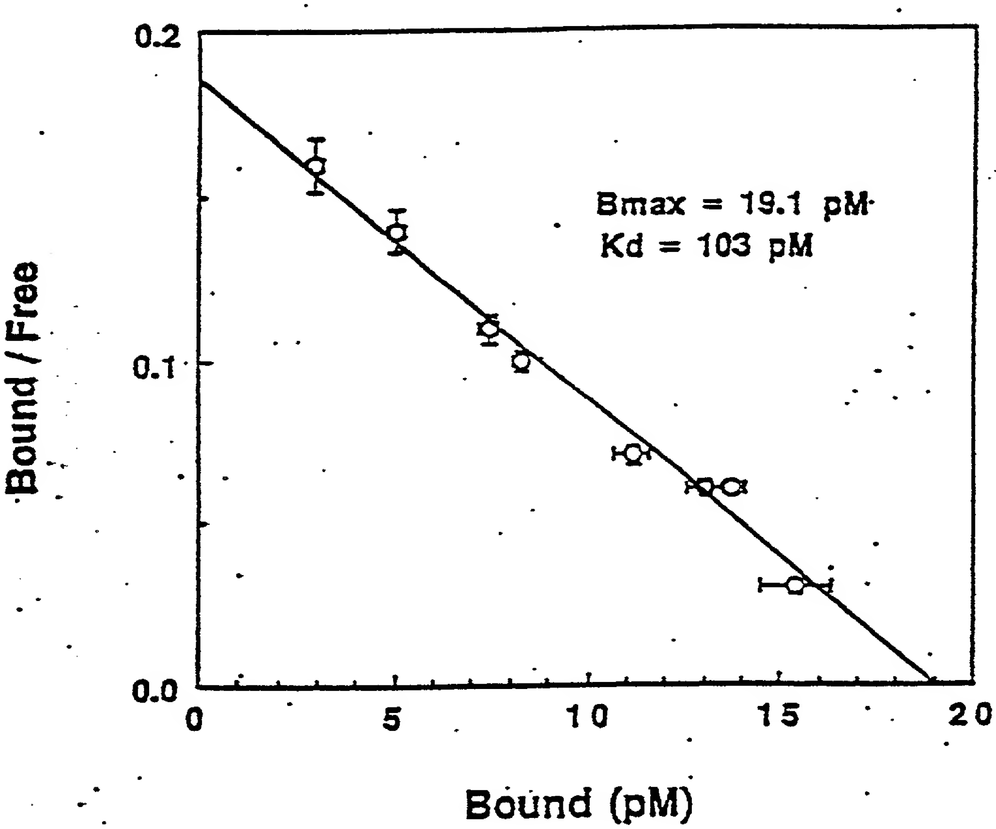
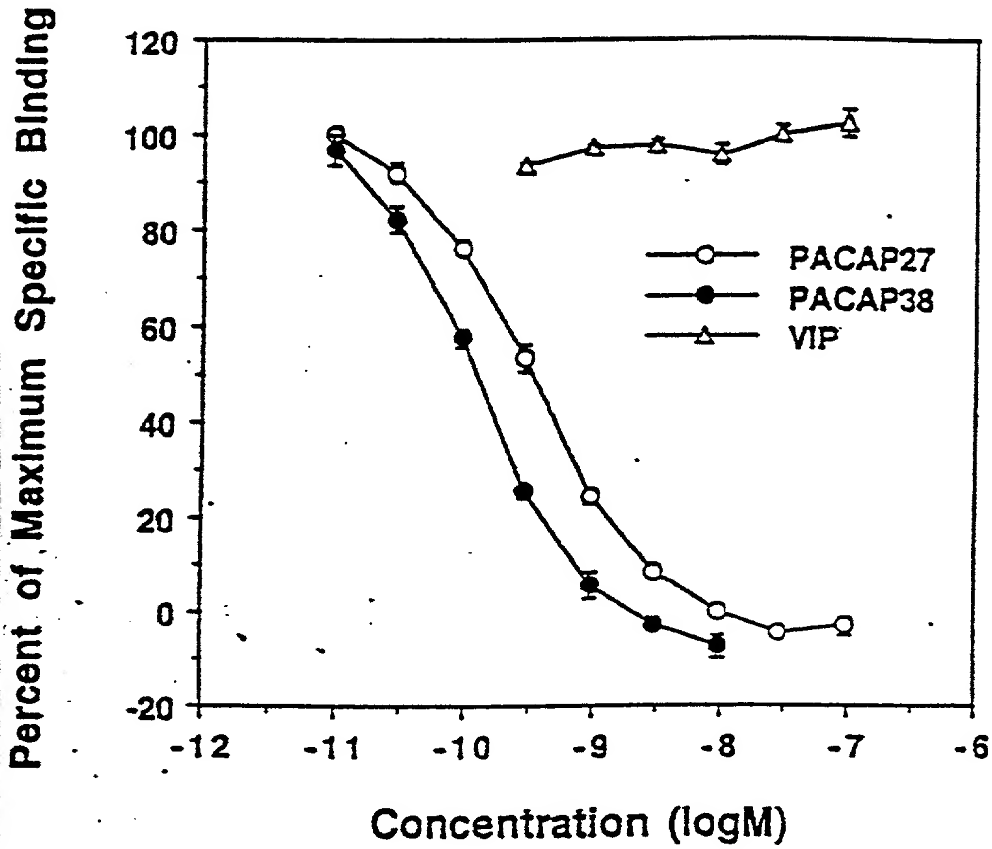
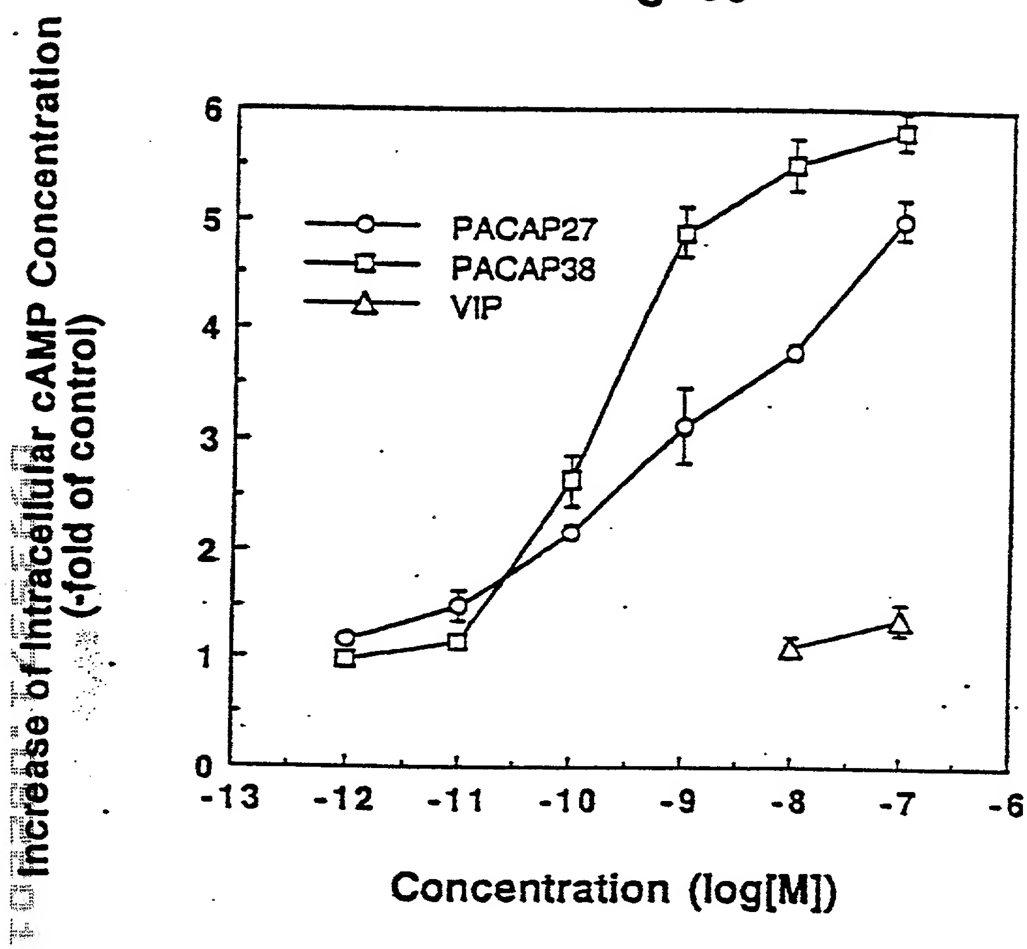


Fig. 35



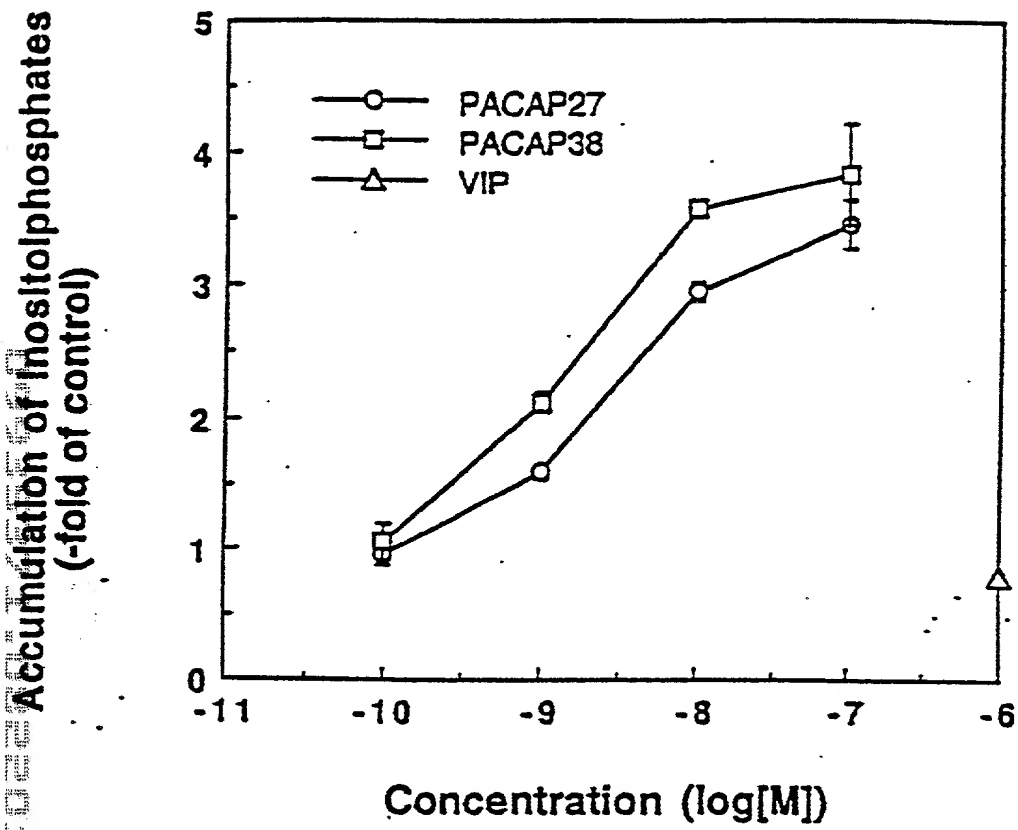
Percent of Maximum Specific Binding
120
100
80
60
40
20
0
-20
-12
-11
-10
-9
-8
-7
-6
Concentration (logM)
PACAP27
PACAP38
VIP

Fig. 36



Increase of Intracellular cAMP Concentration
(-fold of control)
0
1
2
3
4
5
6
PACAP27
PACAP38
VIP
-13
-12
-11
-10
-9
-8
-7
-6
Concentration (log[M])

Fig. 37



Accumulation of Inositolphosphates
(-fold of control)
PACAP27
PACAP38
VIP
5
4
3
2
1
0
-11
-10
-9
-8
-7
-6
Concentration (log[M])

Fig. 38

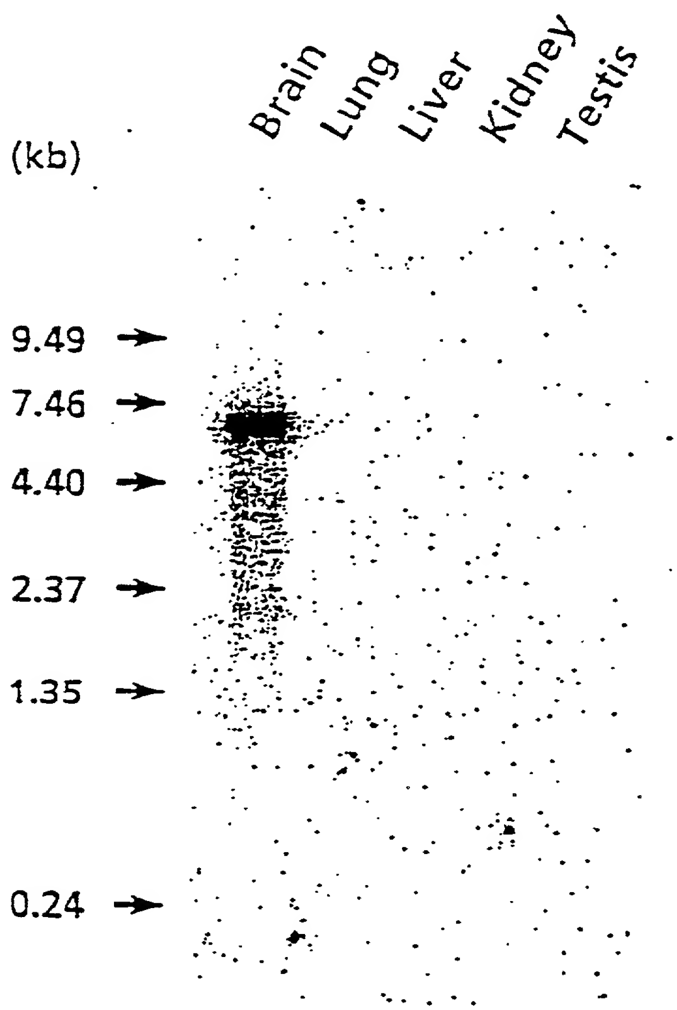
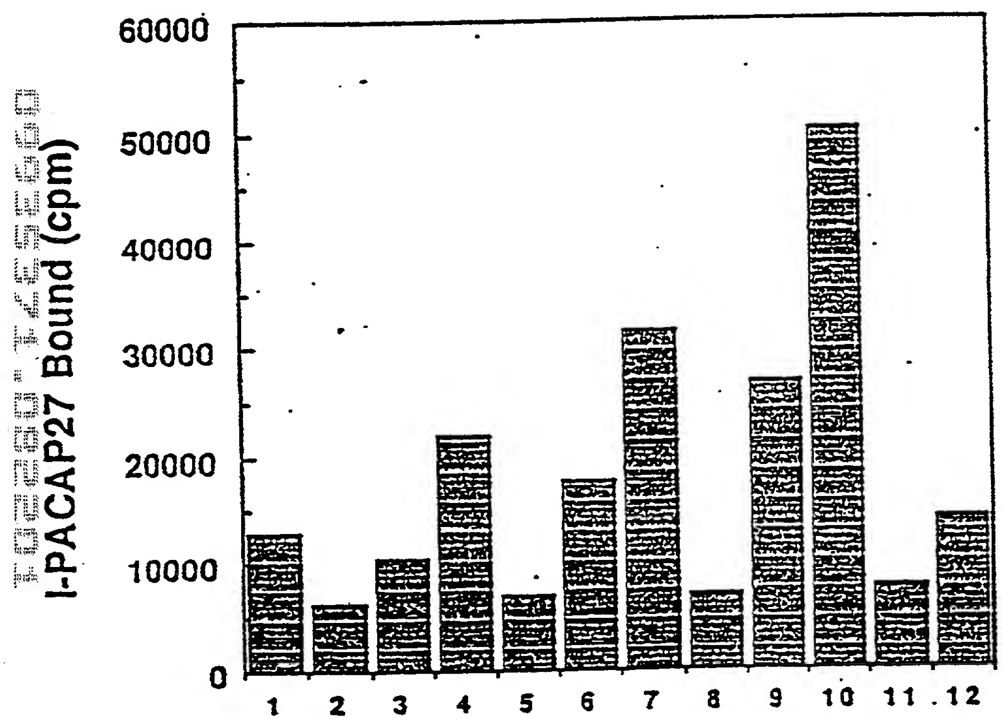


Fig. 39



I-PACAP27 Bound (cpm)
60000
50000
40000
30000
20000
10000
0
1
2
3
4
5
6
7
8
9
10
11
12

Fig. 40

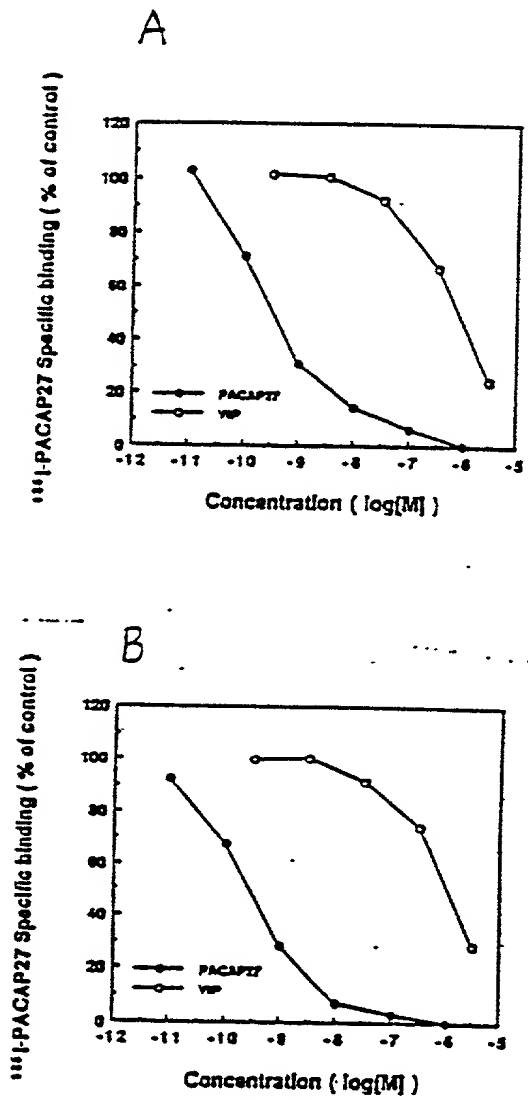

A
¹²⁵I-PACAP27 Specific binding (% of control)
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
PACAP27
VIP
Concentration (log[M])
B
¹²⁵I-PACAP27 Specific binding (% of control)
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
PACAP27
VIP
Concentration (log[M])

Fig. 41

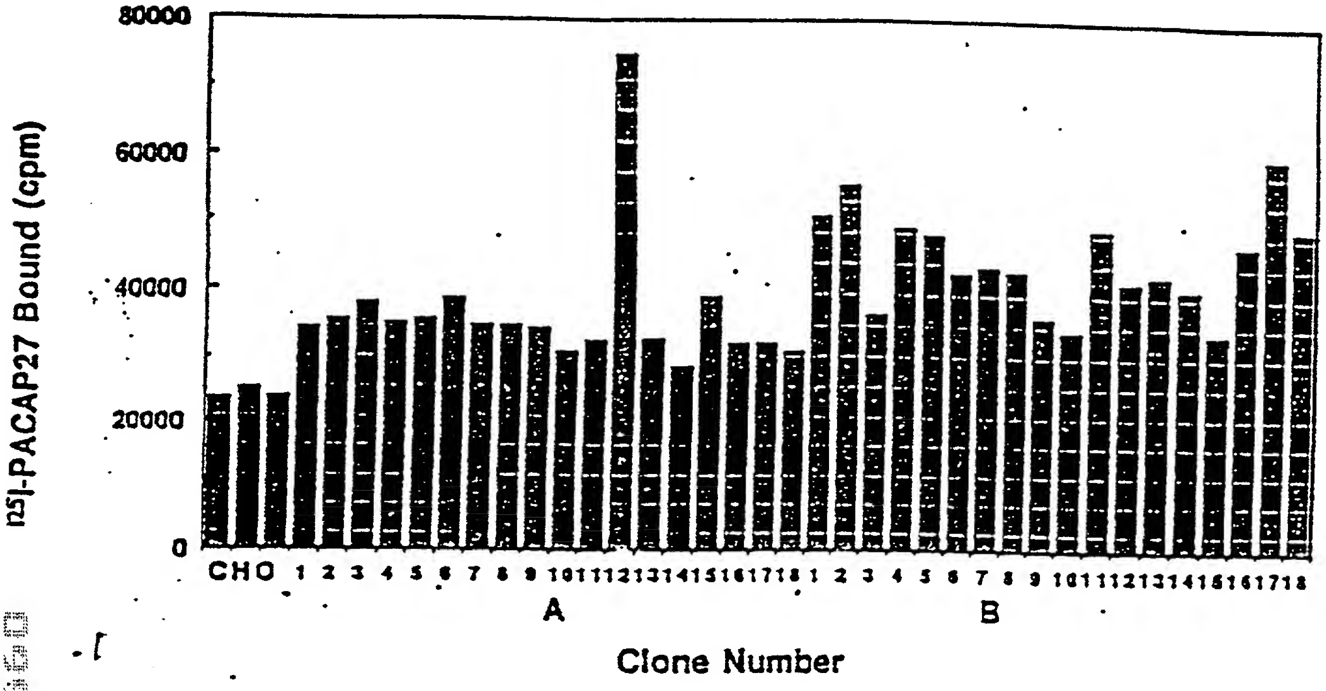

80000
60000
40000
20000
0
125I-PACAP27 Bound (cpm)
CHO 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
A
B
Clone Number

Fig. 42

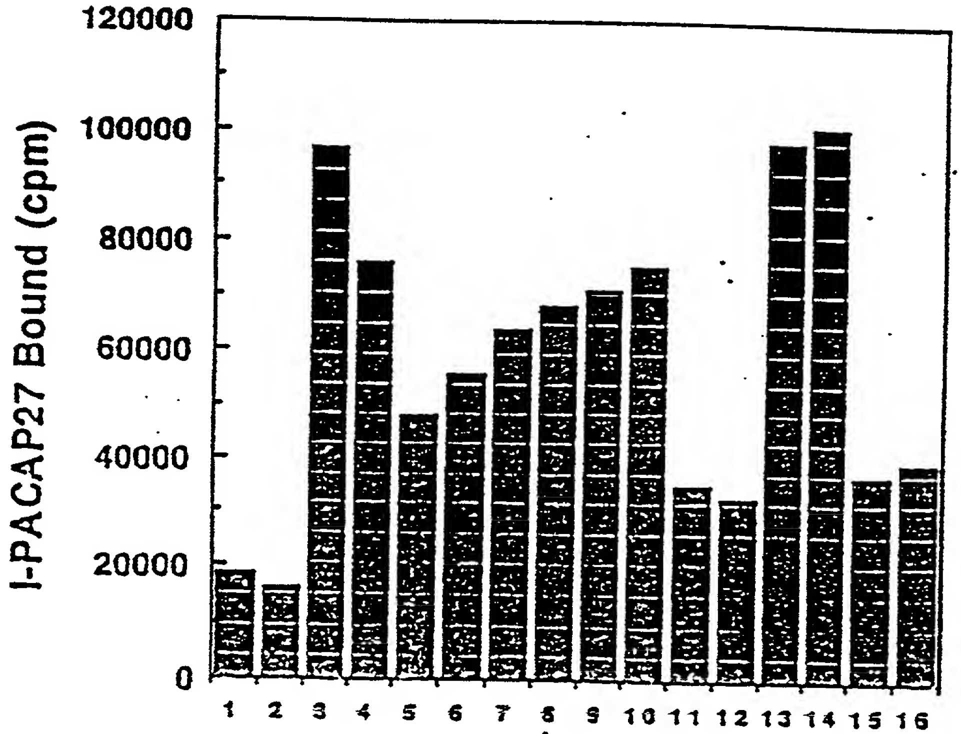
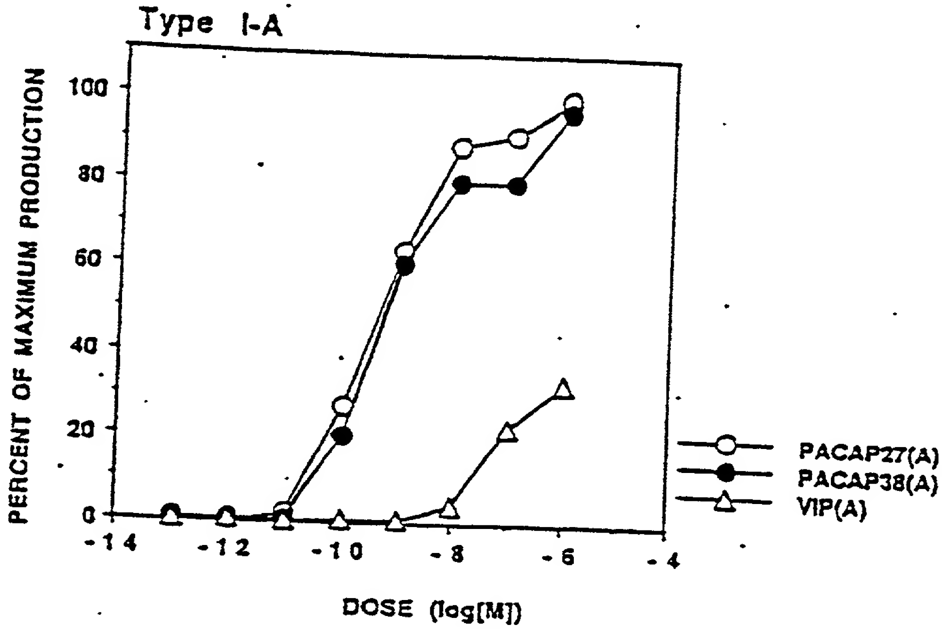

120000
100000
80000
60000
40000
20000
0
I-PACAP27 Bound (cpm)
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

Fig. 43

No. ....


Type I-A
PERCENT OF MAXIMUM PRODUCTION
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
DOSE (log[M])
PACAP27(A)
PACAP38(A)
VIP(A)

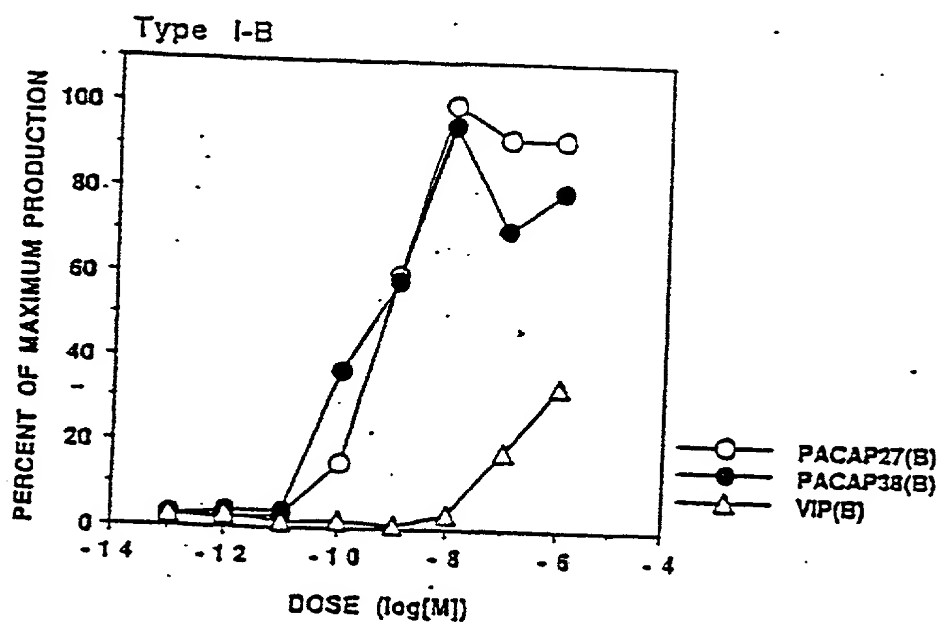

Type I-B
PERCENT OF MAXIMUM PRODUCTION
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
DOSE (log[M])
PACAP27(B)
PACAP38(B)
VIP(B)

Fig. 44

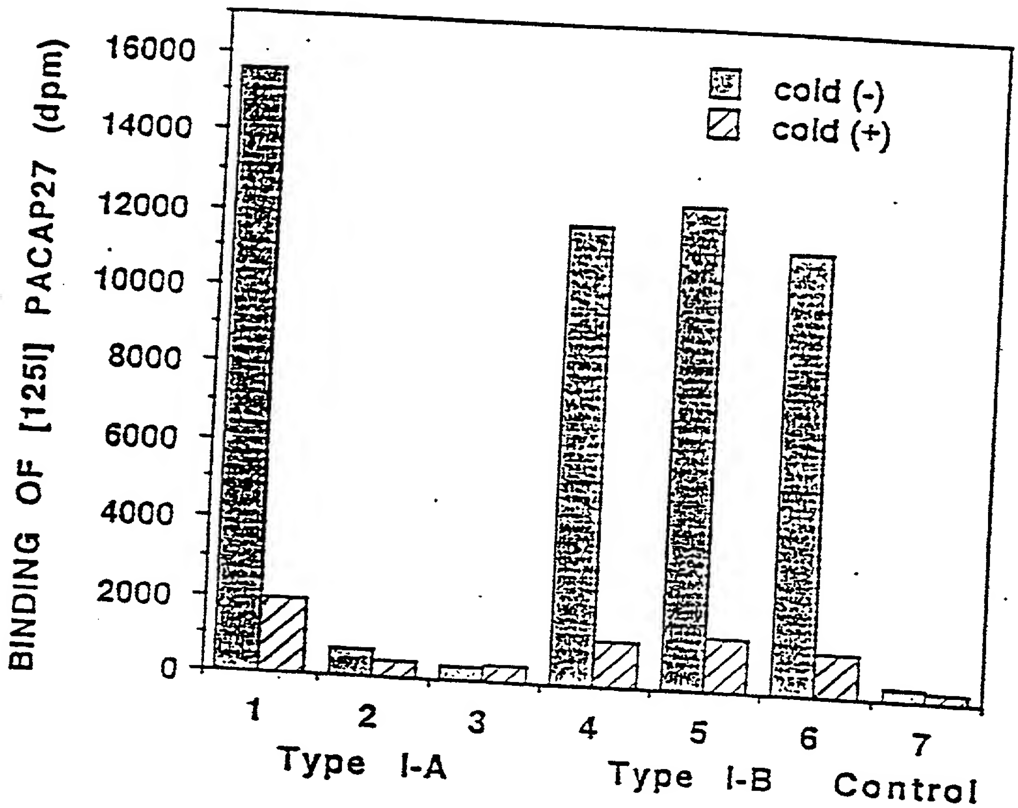
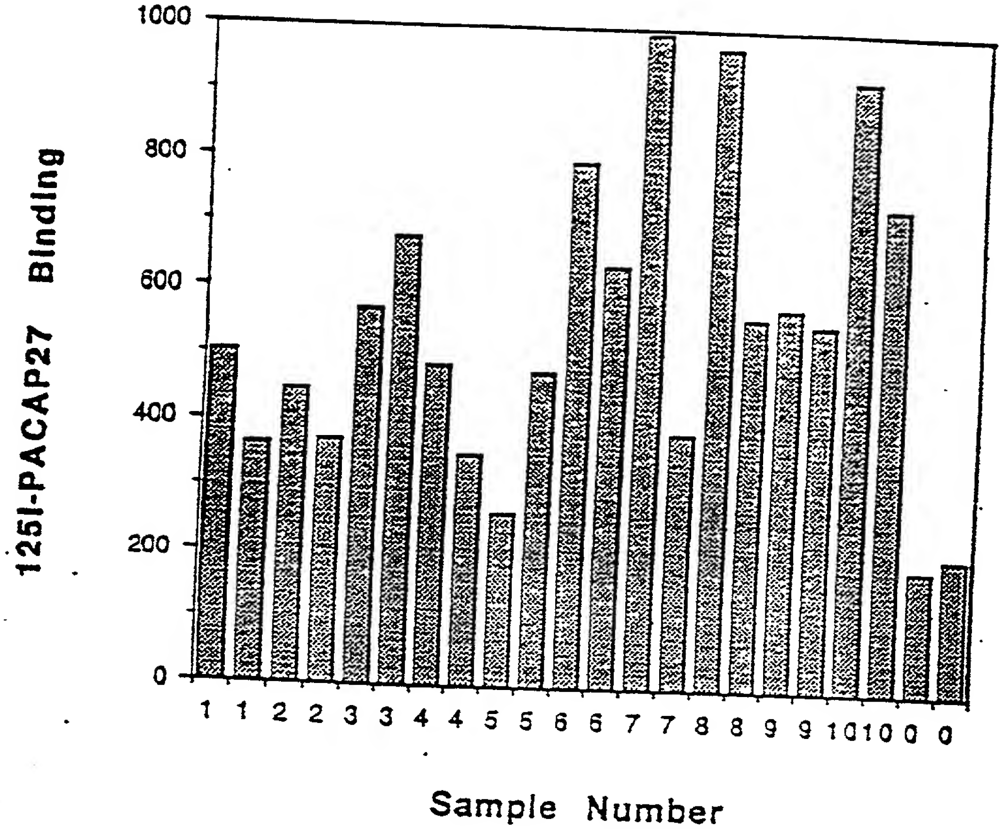

BINDING OF [125I] PACAP27 (dpm)
16000
14000
12000
10000
8000
6000
4000
2000
0
cold (-)
cold (+)
1
2
3
4
5
6
7
Type I-A
Type I-B
Control

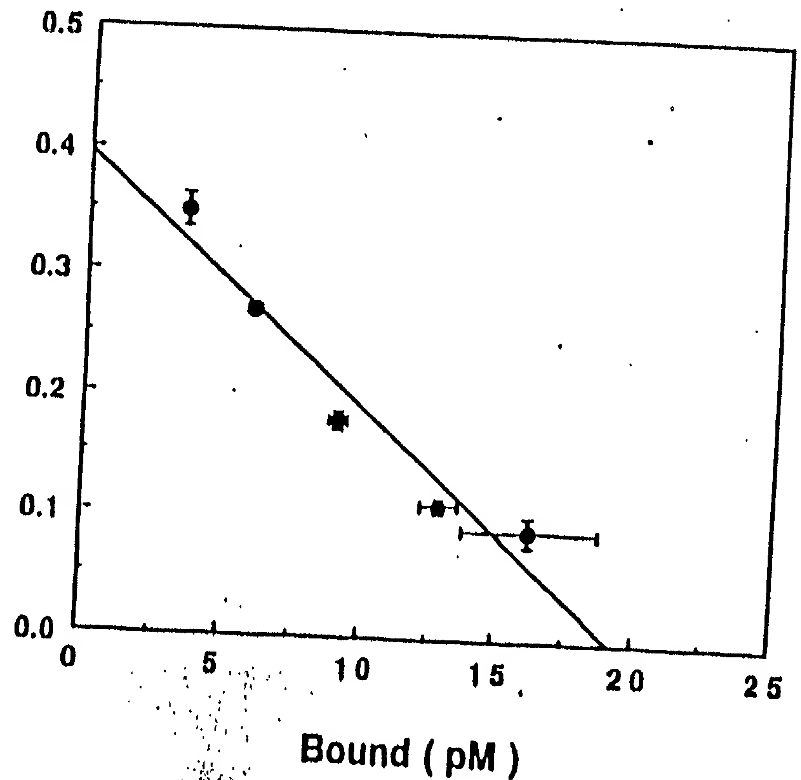
Fig. 45



1000
800
600
400
200
0
125I-PACAP27 Binding
1 1 2 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 0 0
Sample Number

A

Fig. 46



B

Fig. 47

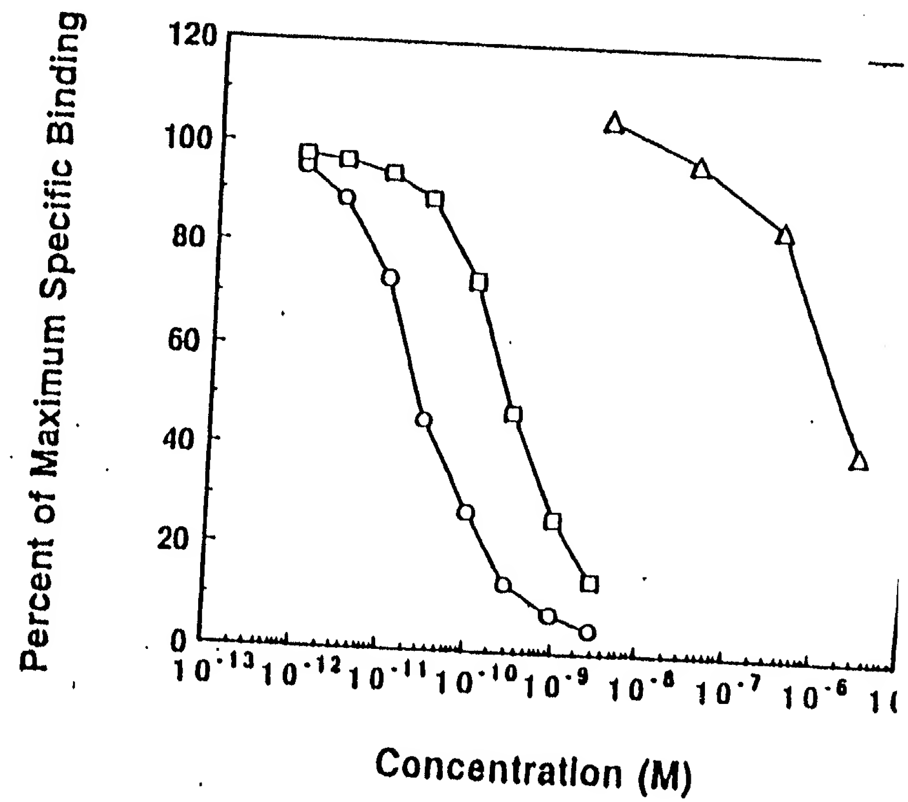


Fig. 48

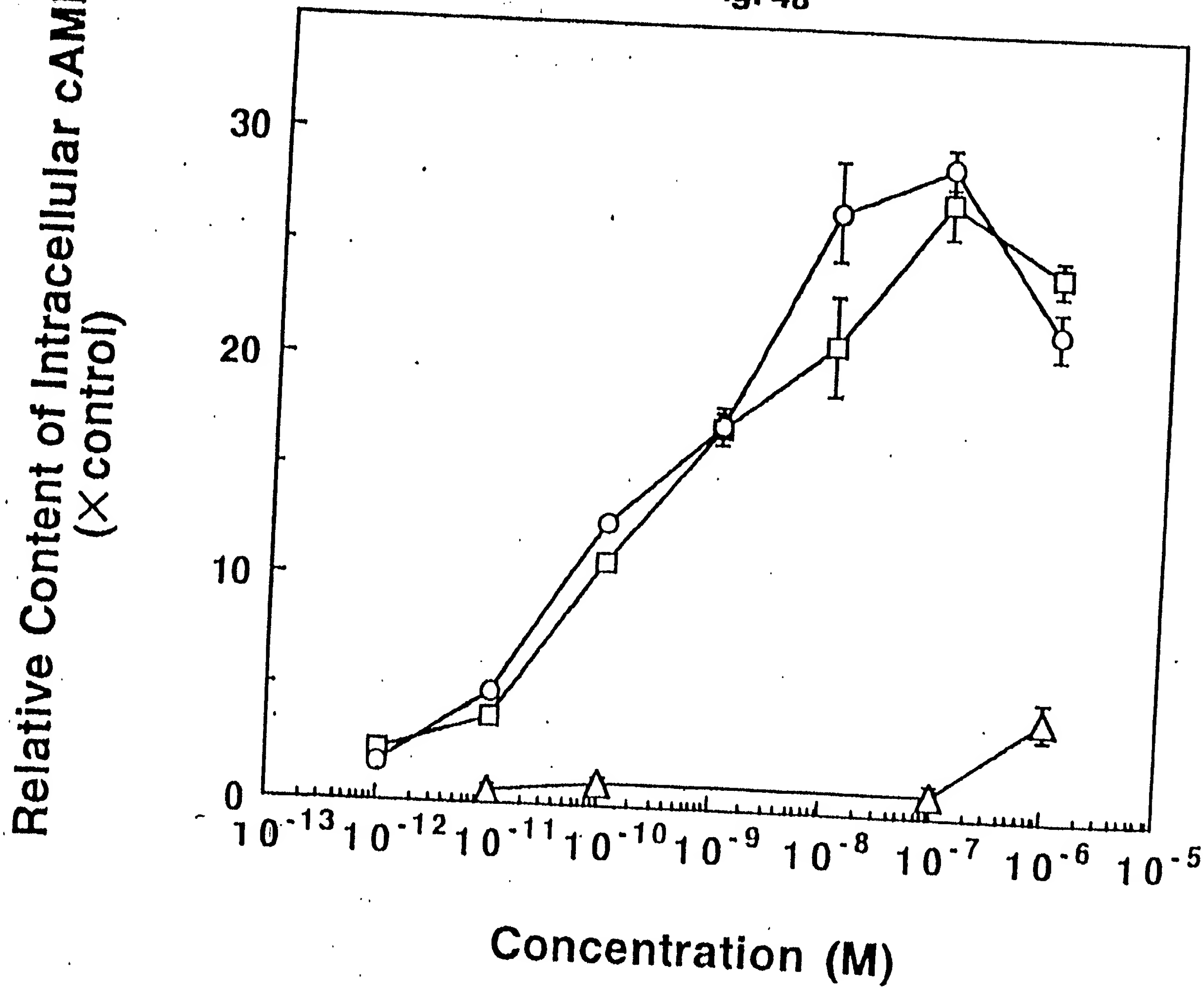
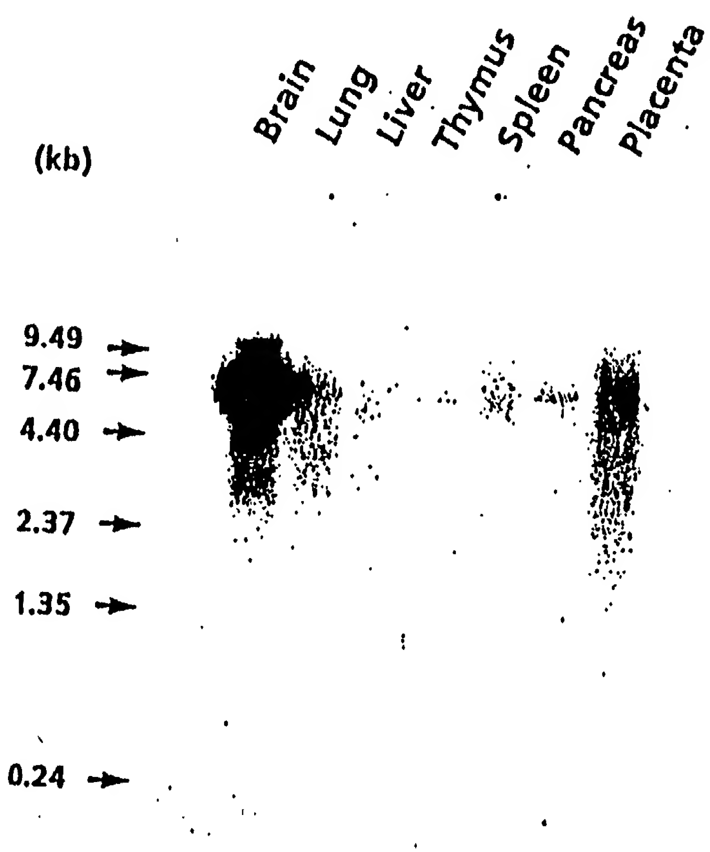
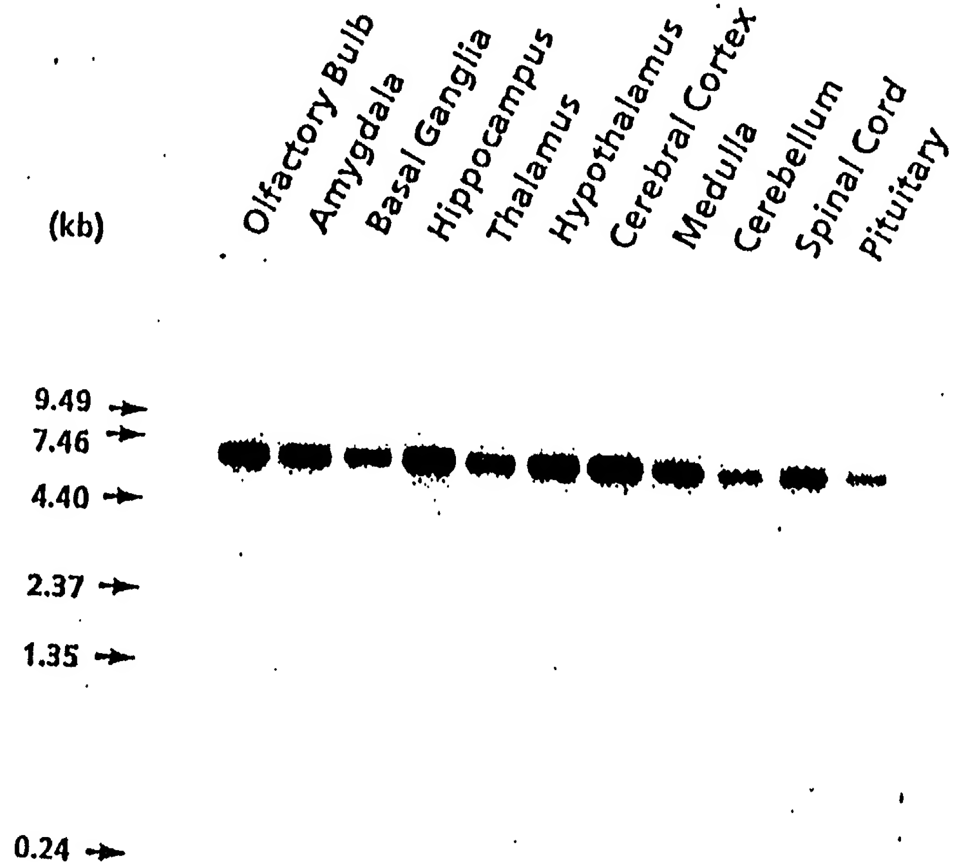

Relative Content of Intracellular cAMP
(× control)
30
20
10
0
10^{-13}
10^{-12}
10^{-11}
10^{-10}
10^{-9}
10^{-8}
10^{-7}
10^{-6}
10^{-5}
Concentration (M)

Fig. 49



(kb)
Brain
Lung
Liver
Thymus
Spleen
Pancreas
Placenta
9.49
7.46
4.40
2.37
1.35
0.24

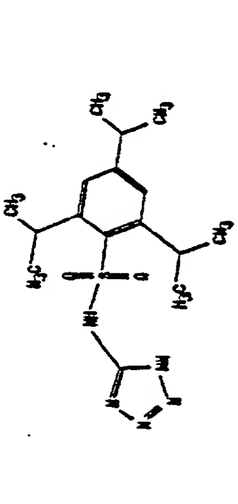
Fig. 50



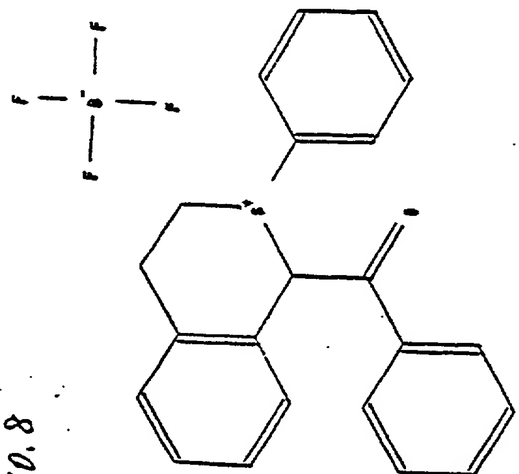
(kb)
Olfactory Bulb
Amygdala
Basal Ganglia
Hippocampus
Thalamus
Hypothalamus
Cerebral Cortex
Medulla
Cerebellum
Spinal Cord
Pituitary
9.49
7.46
4.40
2.37
1.35
0.24

Fig. 51-2

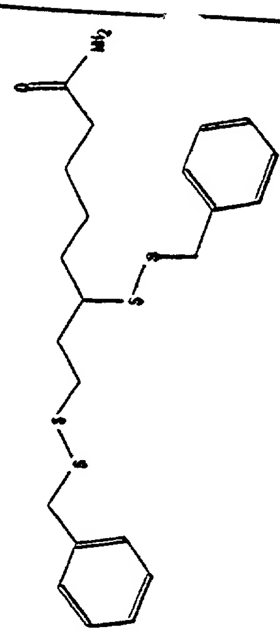
NO.7



NO.8



NO.9



NO.10

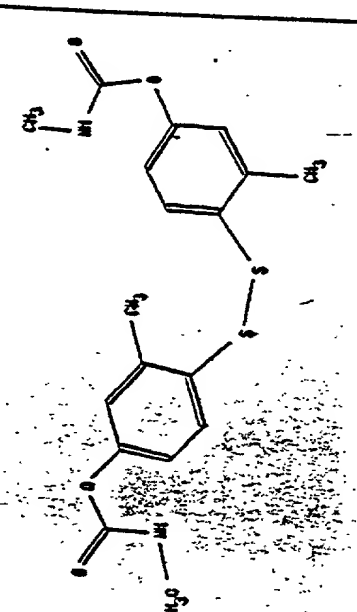
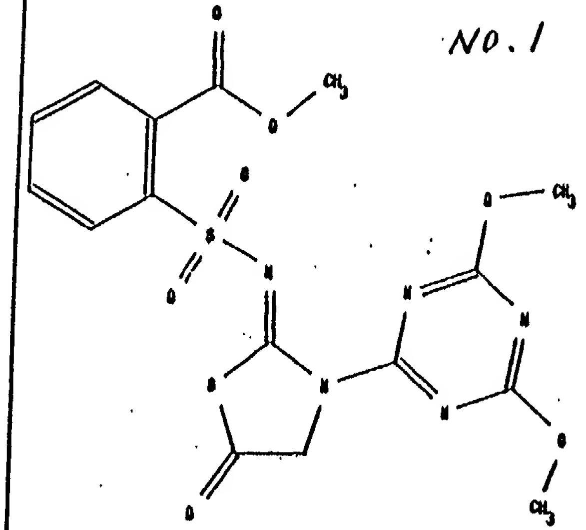
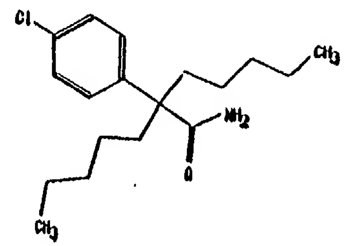


Fig. 31-1

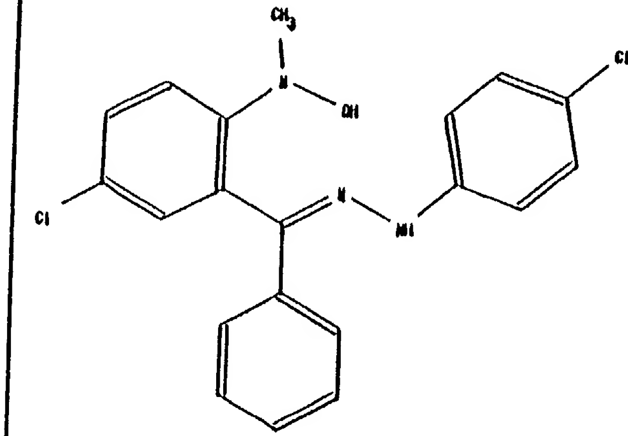
NO. 1



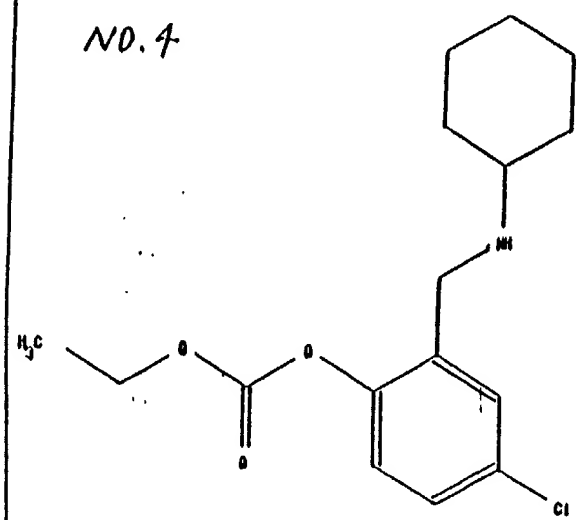
NO. 2



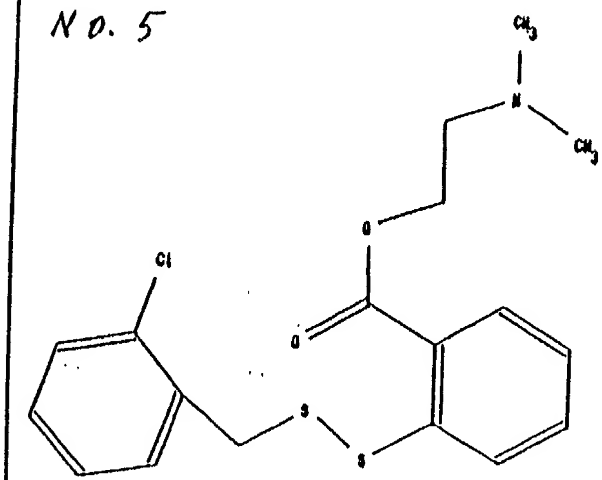
NO. 3



NO. 4



NO. 5



NO. 6

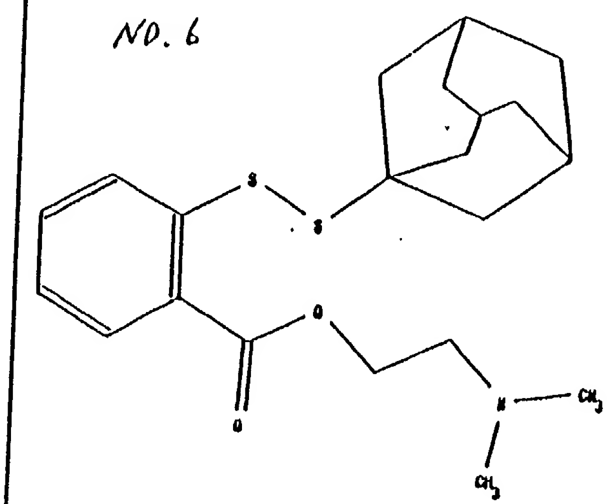


Fig. 52

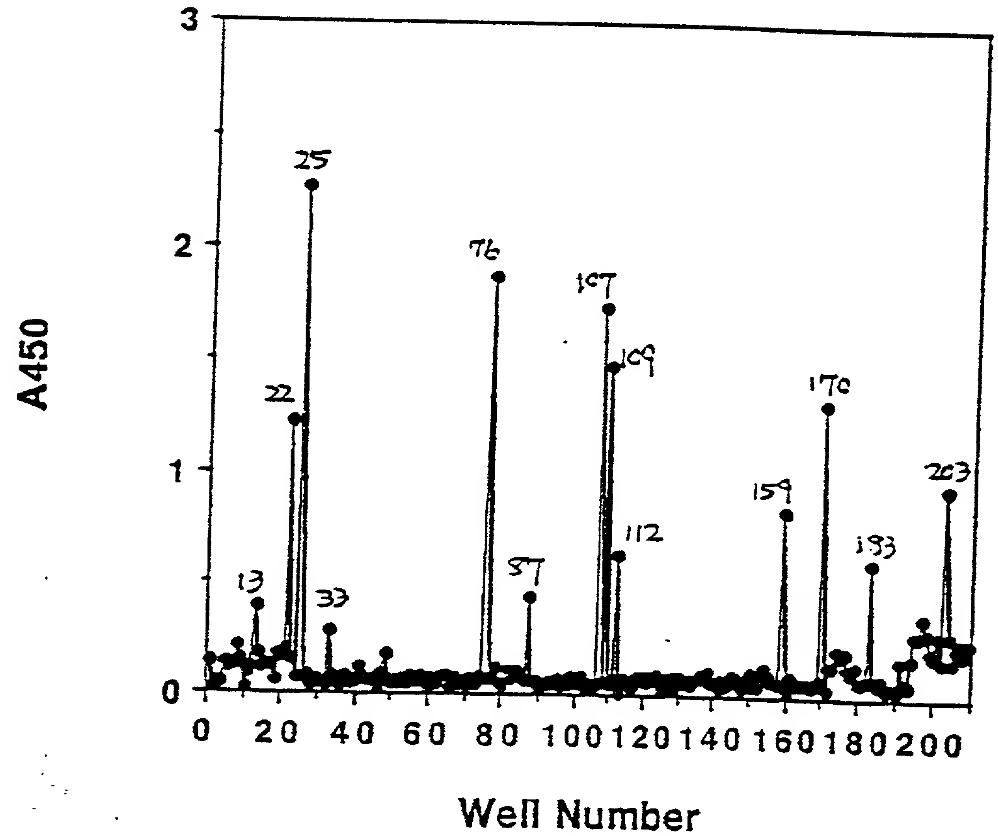

A450
3
2
1
0
25
76
107
109
22
170
159
203
112
183
87
13
33
0 20 40 60 80 100 120 140 160 180 200
Well Number

Fig. 53

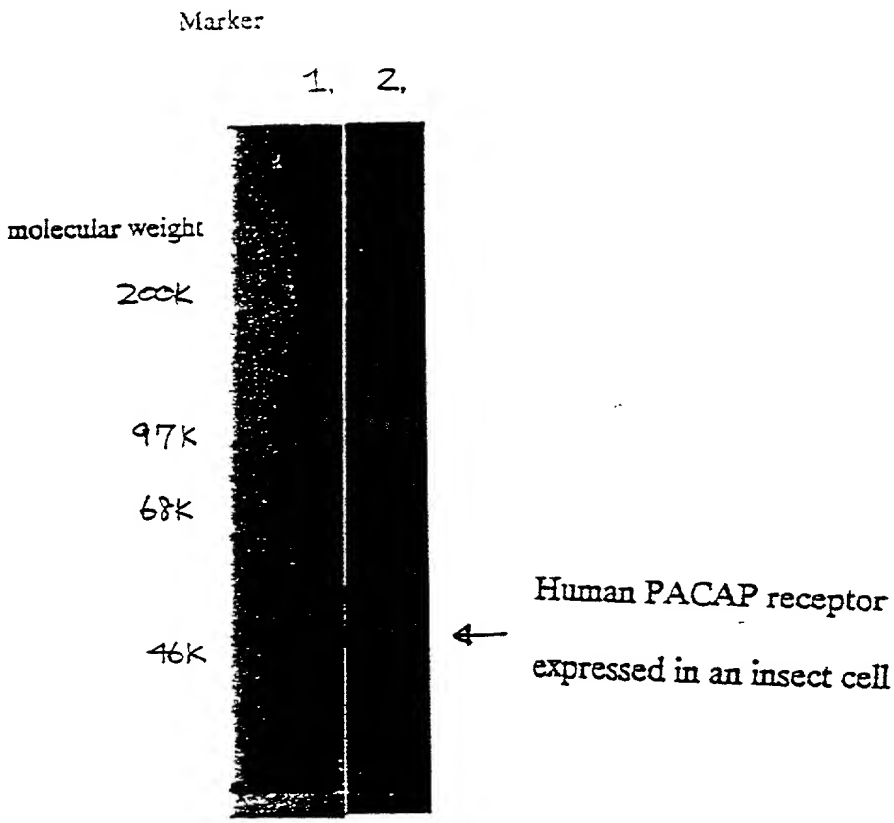
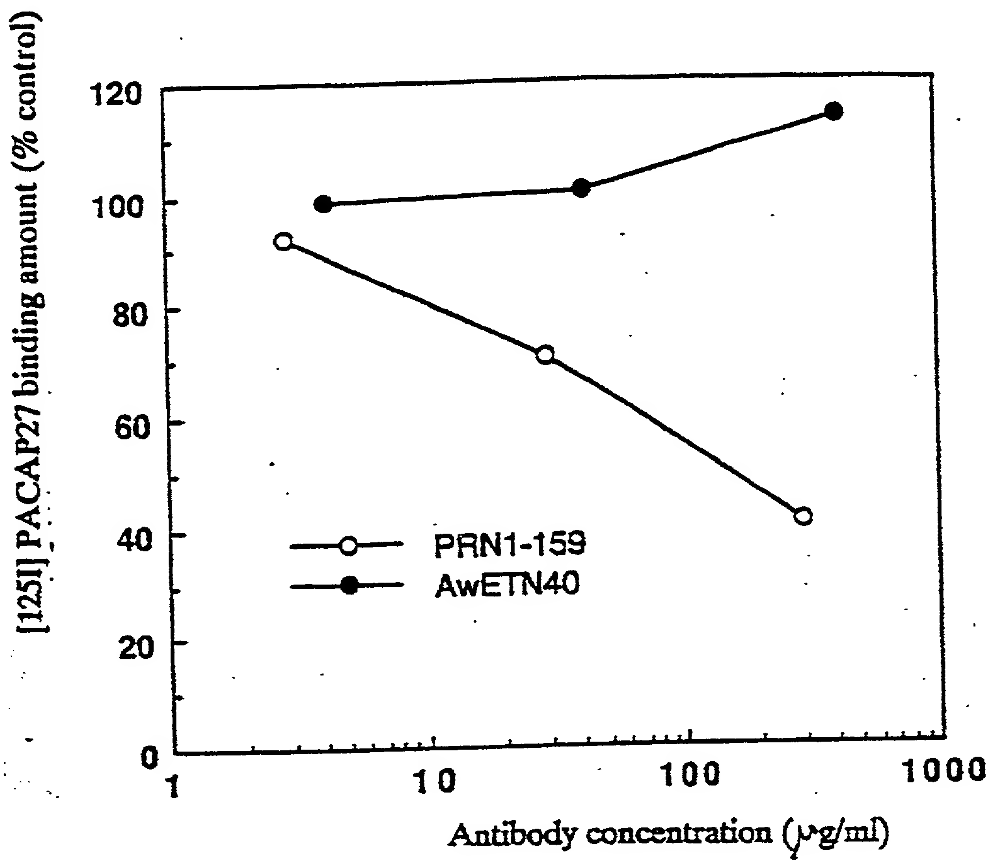

Marker
1.
2.
molecular weight
200K
97K
68K
46K
Human PACAP receptor
expressed in an insect cell

Fig. 54


[125I] PACAP27 binding amount (% control)
120
100
80
60
40
20
0
PRN1-159
AwETN40
1
10
100
1000
Antibody concentration (μg/ml)